STIC-Biotech/ChemLib

From:

Sent: To: Subject: Kaushal, Sumesh Tuesday, May 03, 2005 5:45 PM STIC-Biotech/ChemLib

10657852: SEQ search

10657852: SEQ search Please search

SEQ ID NO:3

SEQ ID NO:15

S. Kaushal

AU1636, REM2.B85 Ph: 571-27-20769 Mail Box: REM2.C70

STAFF USE ONLY	
Searcher: Searcher Phone: 2- Date Searcher Picked up: Date Completed: Searcher Prep/Rev. Time: Online Time:	

Type o	of Search
NA#:	AA#:
Interference:	SPDI:
S/L:	Oligomer:
Encode/Trans	sl:
Structure#:_	Text:
inventor:	Litigation:

Vendors and cost where applicable STN:___ DIALOG:_ QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM:__(WWW/Internet:_ Other(Specify):_

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STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 102494

TO: Sumesh Kaushal Location: rem/2b85/2c70

Art Unit: 1636

Wednesday, May 11, 2005

Case Serial Number: 10/657852

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Kaushal,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

9, 2005, 20:12:52 ; Search time 65 Seconds (without alignments) 2103.464 Million cell updates/sec

US-10-657-852A-15 1385 1 MPEYWAKCCMLLVFLGFILQ.....NTVSGSNHIVSGSNKVVTDG 267

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	tion	O9m3w4 lolium pere	Q8h3w8 oryza sativ			Q62kn5 burkholderi	O9znx4 petunia hyb	Q81pb4 daucus caro				O9fgq5 arabidopsis	Q69kc3 oryza sativ		Q66cj0 yersinia ps	Q75gm9 oryza sativ	Q67it7 oryza sativ	Q89j37 bradyrhizob	Q9c9h7 arabidopsis	067tw5 oryza sativ		Q9srl7 arabidopsis	_	Q8zgb5 yersinia pe	_	Q91964 moraxella c	Q6z0a9 oryza sativ		Q8i4z3 plasmodium	_	Q9svnl arabidopsis	Q7xpi3 oryza sativ
		! ! !																														
SUMMAKIES	QI.	Q9M3W4	Овнзмв	Q9FN37	0630Н1	Q62KN5	Q9ZNX4	PSKR_DAUCA	Q66Q <u>A</u> 4	9н6260	Q940M7	Q9FGQ5	Q69KC3	Q84NG8	Q66CJ0	Q75GM9	Q671T7	Q89J37	Q9C9H7	Q67TW5	Q6ZGM3	Q9SRL7	PSKR_ARATH	Q8ZGB5	О6К9 D3	Q9L964	Q6Z0A9	Q9LS79	Q814Z3	O9LDG0	UNAS60	Q7XPI3
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æ	Query Match	38.3	. 18.9	18.7	16.0	15.7	15.3		14.5	14.4	14.3	14.3	14.2	14.1	14.0	14.0		•	13.9	•	٠	<u>.</u>	щ	ë.	m.	٠	•	ά.	13.5	13.4	13.4	13.4
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Q9sct4 arabidopsis Q6z3t9 oryza sativ										
Q9SCT4 Q6Z3T9	Q67IT2 09XD54	Q6ET59	QBLKV9 Q9M9X1	Q9LGI5	Q6R2J8	QBLJI9	Q6K213	Q69P46	Q8L7L6	Q9ZUK3
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836 380	1051	718	653 883	1065	703	966	1047	1080	983	983
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184.5	183.5	181.5	181	181	180.5	180	180	180	179.5	179.5

ALIGNMENTS

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCLFLSLVALFALLPPPPAAAAPCHPEDLLALRAFAGNLSAGGGGAGLRAAWSGDACCAW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 ------GGISALLAAVSLRTANLSSNLINDTLLDLAALPHLSAFNASNNSLSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGT-----NNSVGSGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KCCML-LVFLGFILQVAGATSWSCHHDDLHALRGLAENLS-GKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
DNA Res. 4:401-414(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98162728; Pubmed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.
                                                                                                                       InterPro; IRR07090; LRR plant.
InterPro; IRR07090; LRR plant.
InterPro; IRR07019; Prot kinase.
InterPro; IRR07019; Prot kinase.
Pfam; PR00650; LRR plane; 1.
Prints; PR00019; LEURICHRPT.
PROSTIE; PS00107; PROTEIN KINASE AIP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE SI; 1.
PROSITE; PS00108; RECTEIN KINASE SI; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                     clone:POS85H11.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP004342; BAC20742.1; --
                         Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                                             18.9%; Score 262; DB 2; Length 10
40.1%; Pred. No. 5.5e-11;
ive 19; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  1010 AA; 109074 MW; 5CCB04E51E18AF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative receptor protein kinase.
Name=At5953890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1036 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 40.1
1es 71; Conservative
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                                                                                                                P36897; 1IAS.
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SEQUENCE FROM N.A.

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CEGSDVSGRVTKLVLPEKGLEGVISKSLGELTELRVLDLSRNQLKGEVPAEISKLEQLQV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 KSLTTDSQSLGMGSI-NMLLHVSSRRTLDEEPNTISGTNNSVG-----SGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 NDNTVV----SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG-----
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninol P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Rawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Theologis M., Southwick A., Shinozaki K., Davis R.W., Ecker J.R. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROW N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang B., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Bakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theelogis A.; Shouthwick A., Shinozaki K., Shinitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

L. Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AX064019; AAL36375.1; -.

EMBL; AX064019; AAL36375.1; -.

EMBL; AX064019; AAL36375.1; -.

EMBL; AX064019; P:Protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein aerivity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIRELEQLSLSGNY--LSGE---LSKNLSNLSGLKSLLISENRFSDVIPD 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.7%; Score 258.5; DB 2; 30.7%; Pred. No. 1e-10; iive 50; Mismatches 98;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
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Pfam; PF00069; Pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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ID Q6
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Pfam; PF00560; LRR 1; 8. PRINTS; PR00019; LEURICHRPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 IPSSIGELDHLRYLDLSGNSLVGEVPKSLQ------IRLKSLTTDSQSLGMGSIN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 TPVLLTNVAAGKIAATSTDAVNGSQLYTLQQEFSQQYDLLTSQVSSLSTSVSGL-QGSVS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 MLLHVSSRRTLDEEPNTISGTN-----NSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 VVTGSDNTVVGS--------NHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSG 238
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 ALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKR-----GLGGI
                                                                                                                                                                                                                                                                                                      A Holden W. Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., A Holden W. Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Benthal E., Sebaihia M., Thomson N.R., Bascon N., Beacham I.R., Brooks K., Brown N.R., Crosset B., Chaliss G.L., Cherevach I., Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D., Relthwell T., Praser A., Hance Z., Hauser H., Holroyd S., Jagels K., A Rabbinowitsch B., Rutherford K., Sanders M., Simmonds M., Sambinowitsch B., Rutherford K., Sanders M., Simmonds M., Simmonds M., Stephonowitsch B., Rutherford K., Sanders M., Simmonds M., Genomic plasticity of the causative agent of melioidosis, Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; Genomic plasticity of the causative agent of melioidosis, Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

R BMBL; BX571965; CAH35630 Li. -

R SEQUENCE 1124 AA; 104844 WW; 90EC4527E9017602 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Burkholderiaceae; Burkholderia.
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                           Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 EHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 TNSTASGDNSTASGTNASASGENSTAT 566
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                                                                        Putative outer membrane protein.
ORFNames=BPSL1631;
                                                                                                                       Burkholderia pseudomallei K96243
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                   STRAIN=K96243;
PubMed=15377794;
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Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Zhou L., Frager C.M.;
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PubMed=15272880; DOI=10.1111/j.1365-313X.2004.02162.x;
Guyon V., Tang W.H., Monti M.M., Raiola A., Lorenzo G.D.,
MCCormick S., Taylor L.P.;
"Antisense phenotypes reveal a role for SHY, a pollen-specific leucine-rich repeat protein, in pollen tube growth.";
Plant J. 39:643-654 (2004).
                                                                                                                                              "Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
EMBL; CP000010; AAJ48866.1; -. SEQUENCE 1012 AA; 94758 MW; S3C27D16C62FBBDE CRC64;
                                                                                                                                                                                                                                                                                                                                        Length 1012;
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TISSUE-Germinating petunia pollen treated with kaempferol;
                                                                                                                                                                                                                                                                                                                                                                                                                       72; Indels
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Last annotation update)
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Best Local Similarity 30.9%; Pred. No. 1.1e-07;
Matches 55; Conservative 31; Mismatches 72;
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InterPro; IPR007090; LRR_plant.
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SWISS-PROT
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                                                                                                                                                                                                                                                        -----SNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG
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                                                                                                                     14 FLGFILQVAGAT---SWSCHHDDLHALR----GLAENLSGKGAVRLRAAWSGASCCSWEG
                                                                                                                                                                                                                                                                                                 SINML--LHVSSRRTLDEEPNTISGTNN--SVGSGSNNVVSGNDNTVVSG-----
                                                                                             Gaps
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MISCELLANEOUS: A 36 amino-acid island is present in the 18th
leucine-rich repeat. An island domain has also been found among
the extra-cellular LRRs of the brassinosteroid receptor BRII and
has been shown to be critical for its function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND GLYCOSYLATION. MEDLINE=22025707; PubMed=12029134; DOI=10.1126/science.1069607; Matsubayashi Y., Ogawa M., Morita A., Sakagami Y.; "An LRR receptor kinase involved in perception of a peptide plant hormone, phytosulfokine."; Science 296:1470-1472 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Phytosulfokine receptor precursor (EC 2.7.1.37) (Phytosulfokine LRR receptor kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Receptor with a serine/threonine-protein kinase activity. Receptor with a serine/threonine-protein kinase activity. Regulates, in response to phytosulfokine binding, a signaling cascade involved in plant cell differentiation, organogenesis and sometic embryogenesis.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane
                                                        / Match 15.3%; Score 212; DB 2; Length 353; Local Similarity 24.2%; Pred. No. 8.1e-08; Asservative 50; Mismatches 90; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
TISSUE SPECIFICITY: Expressed ubiquitously in leaf, apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has been shown to be critical for its function.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
                 Potential.
44CEA54EE2595COF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1021 AA
                                                                                                                                                                             VGCETASGRVVALRLPKR-------
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                                                                                                                                                                                                                                                                                                                                                                                                                    225 NDNNVSGSFHTVSG-----EHNTVSG 245
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               21 Pc
38363 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daucus carota (Carrot)
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353 AA;
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                            SEQUENCE
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                                                           Query Match
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a collaboration
        between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             InterPro; IPR000719; Proc kinase.
InterPro; IPR000719; Proc kinase.
InterPro; IPR000871; Ser_thr_pkin_AS.
Pfam; PF000560; LRR; 16.
Pfam; PF00069; Pkinase; 1.
PRODOM; PR000019; LEURICHRPT.
ProDom; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Glycoprotein; Kinase; Leucine-rich repeat; Receptor;
Repeat; Serine/threonine-protein kinase; Signal; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
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It is produced through
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Phytosulfokine r
Potential.
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Protein kinase.
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  entry is copyright.
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19.
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                                                                                       InterPro; IPR011009; Kinase_like.
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                                                                      EMBL; AB060167; BAC00995.1; -. HSSP; Q62838; 1LUF.
                                                                                                         LRR_plant
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1021
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757
771
869
                                                                                               IPR001611;
IPR007090;
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592 55
632 63
1021 AA;
                                                                                                                                                                                                                  Fransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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70 WNAADCCKWEGVIC-SADGTVIDVSLASKGLEGRISPSLGNLTGLLRLNLSHNSLSGGLP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 GHNNLSGNLPGDLFNATSLEYLSFPNNELNGVINGTLIVNLRNLSTLDLEGNNINGRIPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 WSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 KSLQIRLKSLTTDSQSLGMGSINML-------LHVSSRRTLDEEPNT-- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 -----ISGINNS-VGSGSNNVVSGNDN-TVVSGNNNHVSGS------NNTVVTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KKCSNRCPIDPLRFNLAPALLILISLASPTS-SCTEQERSSLLQFLSSLSSDGGLAV-SW 69
                                                                                                                                                                                                                                                                                                                                                       7 KCCMLLVFLGF------ILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NHNASGT----KHIVT----DNNNV-----
                                                                                                                                                                                                                                                                                                   98; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicacees, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 SIGQLKRLQDLHLGDNNISGELPSALSNCTHLITINLKRNNFSGNLSNVNFSN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Ronining C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.B., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 -----VSGNDNNVSGSF----H--TVSGEHNTVSGSNNTVSGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 784;
                                                                                                                                                                                                                                              Length 1065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative disease resistance protein; 69620-67266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.4%; Score 199.5; DB 2; Best Local Similarity 24.2%; Pred. No. 1.9e-06; Matches 80; Conservative 51; Mismatches 80;
SMART; SM00169; LRR TYP; 8.
SMART; SM00210; S_TKC; 1.
SMART; SM0019; TYPKC; 1.
PROSITE; PS50011; PROTEIN KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                           Query Match
14.5%; Score 201; DB 2;
Best Local Similarity 24.6%; Pred. No. 2.1e-06;
Matches 87; Conservative 54; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 AA
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 SDNTVVGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                Kinase; Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                               SEQUENCE
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                                                                                     14;
                                                                                                                                                                                                                                                                             S9 FSSNCCDWVGISCKSSVSLGLDDVNESGRVVELELGRRKLSGKLSGESVAKLDQLKVLNLT 118
                                                                                                                                                                                                                                                                                                                                                                                   119 HNSLSGSIAASLLNLSNLEVLDLSSNDFS---GLFPSLINLPSLRVLNVYENSFHGLIPA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 -GASCCSWEGVGCETA-----SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLS 106
                                                                                                                                                                                                                                                                                                                                                     107 GNSLVGEVPKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISG---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TNN------SVGSGSNNVVSGNDNTV--VSGNNNHVSG------SNNTVV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 TGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTV-----SGEHNTVS 244
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                                                                                                                                                                                               28
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He G.M., Li K.G., Yang J.S.;
"Oryza sativa (indica cultivar-group) chromosome 2 genomic sequence.";
submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         10 MLLVPLGPILQ--VAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS----
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     He G.M., Li K.;

"Isolation and expression pattern of putative LRR (leucine-rich repeat) receptor-like kinase in rice.";

"Isolation and expression pattern of putative LRR (leucine-rich repeat) receptor-like kinase in rice.";

"Submitted (ANG-2004) to He EMBL/GenBank/DDBJ databases.

"RMBL; AY73046; AAU12611.1;

"RMBL; AY71494; AAU12611.1;

"RMBL; AY71494; AAU12603.1; -..

"GO; GO:0004872; P:receptor activity; IEA.

"RO GO:0004872; P:receptor activity; IEA.

"InterPro; IPR011009; Kinase_like."

"InterPro; IPR001099; Kinase_like."

"InterPro; IPR001999; LRR Diant.

"InterPro; IPR001999; LRR Diant.

"InterPro; IPR001999; LRR Diant.

"InterPro; IPR001999; LRR Diant.

"InterPro; IPR001999; Prot_Hr Diant.

"InterPro; IPR001999; Ser_thr Diant.

"InterPro; IPR001299; Tyr_Diant.

"InterPro; IPR001299; Tyr_Diant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last amotation update)
Putative leucine-rich repeat receptor-like kinase.
Oryza sativa (indica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                     98;
                                    Length 1021;
                                                                                   94; Indels
                              14.7%; Score 204; DB 1; 24.6%; Pred. No. 1.2e-06; iive 56; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1065 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 GS------ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GEMPRSLSNSRSISLLSLRNNTLSGQIYL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00019; LEURICHRPT.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00365; LRR_SD22; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00560; LRR 1; 20.
Pfam; PF00069; Pkinase; 1
                                                                                     81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                     Matches
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223 229

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119 -QIRLKSLTTD-----SQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secuence From M. A. Shinn P., Bowser L., Carninci P., Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chen M. M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida U., Jones T., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narlusaka M., Southwick A., Tang C.J., A Toriumi M., Wallander E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

Small, BAD2654; P. BAD06647.1; --
REMBL, BT001094; AAN46893.1; --
REMBL, BT001094; P. PIPCTEIN kinase activity; IEA.

GO; GO:0004672; F: P: Proctein kinase activity; IEA.

GO; GO:0006468; P: Proctein amino acid phosphorylation; IEA.
                                      SGNDNTVVSGNNNHVSG-----SNNTVVTGSDNTVVGS--NHVVSGTKHIVTDNNNVVS
                                                                          ----TEISLOKNYLSGGIPGGFKSTEYLDLSSNLIKGSLPSHFRGNRLRYFNASYNRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 SGNDNTVVSGNNNHVSG-----SNNTVVTGSDNTVVGS---NHVVSGTKHIVTDNNNVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL---
                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Receptor-like protein kinase (At5967280/K3G17_4).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids_II; Brassicales; Brassicacese; Arabidopsis.
                                                                                                           G-----HUDNNVSGSFHTVSG-----EHNTVSGSNNTVSGSNH 255
                                                                                                                               G-----HDNNVSGSFHTVSG-----EHNTVSGSNNTVSGSNH 255
   124 TELRFLDLSDNHISGALPASFGALSNLQVLNLSDNSFVGELPNTL-GWNRNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 TELRFLDLSDNHISGALPASFGALSNLOVLNLSDNSFVGELPNTL-GWNRNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Katoh T., Asamizu E., Sato S., Nakamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 AA; 82062 MW; 180302F2B7EFF966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 197.5; DB 2; 28.6%; Pred. No. 2.5e-06; ive 34; Mismatches 78;
                                                                                                                                                                                                                                       751 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Kinase; Receptor.
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001611; LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00560; LRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                eurosids II; Bra
NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T.
Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                          175
                                                                                                           224
                                                                                                                                              230
                                      172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 -QIRLKSLTTD-----SQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVV 171
                                     ORDGLLKFRDEFPIFESKSSPWN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Linl J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                        91'PSSIGELDHLRYLDLSGNSLVGEVPKSL----QIRLKSLTTDSQSLG-----MGSINMLL
                                                                                                                                                                                                                                     226 EFRIFFNNFTSLPSD-----LSGFHNLVTFDISA----NSFSGHFPKFLFSIPSL
                                                                                                                                                                                                             142 HVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGS-----
                                                                                                                                                                                                                                                                                   -----NNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY054256; AAL06915.1; -
GO; GO:0005524; F:RTP binding; IEA.
GO; GO:0004672; F:Protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
CMLLVFLGFIL-QVAGATSWSCHHDDLHALRGLAENLSGKGAVRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom; PD00001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
SEQUENCE 751 AA; 82086 MW; EGADAB4370F49689 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.3%; Score 197.5; DB 2
28.6%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                        --VSGEHNTVSGSNNTVSGSNHIVSGSNKV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                    58 GAS-CCSWEGVGCETASGRVVALRLPKR---
                                                                                                                                                                                                                                                                                                                                                                                         272 AWVSMDRNQFSG---PIEFAN--ISSSSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AT5g67280/K3G17 4.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                      CILTIYFSFLIHSLASPSLHFCRHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR011009; Kinase_like.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
Pfam; PF00560; LRR 1; 5.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .-DEC-2001
                                                                                                                                                                                                                                                                                   190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q940M7;
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Matches
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223

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58 GASCCSWEGVGCETA-SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPK 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SL----QIRLKSLTTDSQS----LGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 NVVSGNDNTVVSGNNNHVSG----SNNTVVTG---SDNTVVGSNHVVSGTKHIVTDNN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 TV-----AVPSVARNHVHGQVPPWLGNLTALEDLNMADN--IMSGHVPPALSKLINLRS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PEYMAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW----S
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes."; Genome 46:1084-1097(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY268139; AAP31049.1.

REMIN, AY268139; AAP31049.1.

REGO; GO:0005224; F:ATP binding; IEA.

RO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

RO; GO:0004872; F:receptor activity; IEA.

RO; GO:0016740; F:rensferase activity; IEA.

IN THEPPO; IPR001611; LRR.

IN THEPPO; IPR001611; LRR.

IN THEPPO; IPR001719; Prot. kinase.

R INTERPO; IPR001719; Prot. kinase.

R Pfam; PR00560; LRR 11.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chibbar R.N.,
                                                                                                                                 307 IPESLGHIRTLEILTMSVNNLSGLVPPSLFNISSLTFLAMGNNSLV 352
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                                                                                233 FHTVSGEHNTVS----GSNN-----TVSGSNHIVSGSNKVV
                                                                                                                                                                                                                                                                                                                           01-000-2003 (TrEMBLrel. 24, Created)
01-00N-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%; Score 195.5; DB 2; 30.3%; Pred. No. 5.2e-06; tive 37; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Pubmed=14663527; DOI=10.1139/g03-071;
Gu Y.Q., Anderson O.D., Londeore C.F., Kong X.,
Lazo G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEAM, PROUSEO, LER 1, 17.

PRINTS; PROUD19; LEURICHRPT.

PRODEN; PSOU0001; PROTEIN KINASE; 1.

PROSITE; PSOU107; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PSO0119; PROTEIN KINASE DOM; 1.

PROSITE; PSO0108; PROTEIN KINASE ST; 1.
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                                                                                                                                                                                                                                                                             PRT; 1023
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Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Putative receptor kinase.
                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                             Q84NG8
                                                                                                                                                                                                                       RESULT 13
Q84NG8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 SRSPPRVIAIDLSSEGITGTISPCIANLTSLMTLQLSNNSLHGSIPPKLGLLRKLRNLNL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 MGSINML--LHVSSRRTLDEEPNTIS-----GTNNSVGSGSNNVVSGNDNTVVSG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 NNNHVSG-----SINITVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNSLVGEVPKSL----OIRLKSLTTDS-----OSLG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VFLGFILLQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASC--CSWEGVGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
230 GEIPSGFADEIPEDATVDLSFNQLTGQIPGFRVLDNQESNSFSG-NPGLCGSDH 282
                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AP005966; BAD34184.1; -.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004713; F:Protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 1102; Score 196; DB 2; Length 1102; Local Similarity 24.3%; Pred. No. 5.2e-06; Loses 84; Conservative 47; Mismatches 109; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILNTS; PRO0019; LEURICHET.

PILNTS; PRO0019; LEURICHET.

PRODOM; PD000001; Prot Kinase; 1.

SMART; SM00220; TYKC; 1.

SMART; SM00219; TYKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATF; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Hypotherical protein; Kinase;

ATP-binding; Hypotherical protein; Kinase;

SEQUENCE 1102 AA; 119984 MM; B960CDE45175C68E CRC64;
                                                                                                                                                                                                                 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1047H05.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR011009; Kinase_like.
InterPro; IPR001001; LRR_plant.
InterPro; IPR007090; LRR_plant.
InterPro; IPR007019; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TAS-GRVVALRLPKRG-----
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00560; LRR 1; 2.
Pfam; PF00069; Pkinase;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
105-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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622 AA; 65230 MW; 30B8C7D77A3D73CD CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative exported protein precursor.
ORFNames=YPTB1413;
     LTVA - - INNLQGLIPPVLFNMSSLECLNFGSNQLSGS 263
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                                                                                                                                                                                                                                                                                      622 AA
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234 TGLSSLGAGGNALAGELPGWIGEMAALETLDLSGNRFVGAIPDGISGCKNLVE----VD 288
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Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chow T.-Y., Hsing Y.-I.C., Chang S.-J., Chen H.-C., Chen S.-K.,
Chen T.-R., Chen Y.-L., Chang C.-H., Chung C.-I., Has S.-Y.,
The Hsiao S.-H., Hsiung J.-M., Hsu C.-H., Kau P.-I., Lee M.-C.,
Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Mu H.-P., Shaw J.-F.;
EMBL, AC144737, AAT01367.1;
Co, GO:0004524; F:ATP binding; IEA.
Co, GO:0004674; F:protein serine/threonine kinase activity; IEA.
Co, GO:0004674; F:protein serine/threonine kinase activity; IEA.
Co, GO:0004671; F:protein serine/threonine kinase activity; IEA.
Co, GO:0004713; F:protein-threonine kinase.
Co, GO:0004714; F:protein-threonine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 194; DB 2; Length 91 26.3%; Pred. No. 5.9e-06; tive 43; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0019; LEURICHRPT.
Prodom; PD000001; LER_TYP; 5.
SMART; SM00219; LTR. TYP; 5.
SMART; SM00219; TYRC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
ATP-binding; Hypothetical procein.
SEQUENCE 917 AA; 96507 MW; AEGDC9F7DD6E0B77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: May 9, 2005, 20:21:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 26.3% nes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GSNNTVSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | ::|
LSGNALTG 296
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 9, 2005, 20:18:45; Search time 16 Seconds (without alignments) 1605.617 Million cell updates/sec

US-10-657-852A-15 1385 1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
!: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	190.5	13.8	1008	2	D84434	probable receptor-
7	190	13.7	622	N	AF0169	probable exported
m	186	13.4	645	~	T05251	
4	184.5	13.3	836	~	T46070	
	179.5	13.0	983	~	G84524	probable disease r
9	176.5	12.7	743	~	C84633	probable disease r
7	173.5	12.5	590	N	B86440	probable protein k
60	169	12.2	420	~	AE1857	hypothetical prote
σ	168.5	12.2	1095	~	G96746	
10	168	12.1	1019	~	C96519	dise
11	164.5	11.9	716	N	H84421	probable receptor-
12	164	11.8	166	N	B85440	receptor kinase-li
13	162.5	11.7	1232	~	T05322	hypothetical prote
14	162	.11.7	773	~	T00502	probable receptor-
15	161.5	11.7	905	~	T00475	probable disease r
16	161	11.6	719	7	T47727	hypothetical prote
17	191	11.6	907	7	A86460	
18	159.5	11.5	768	N	T17462	disease resistance
19	158.5	11.4	658	~	B84664	probable receptor-
20	158	11.4	478	N	H86459	hypothetical prote
21	157.5	11.4	966	N	T10725	protein kinase Xa2
22	157	11.3	241	~	S61925	cyst wall protein
23	156.5	11.3	702	~	A86383	76.4K protein kina
24	156.5	11.3	876	7	D96558	probable protein k
25	156	11.3	371	~	T49908	hypothetical prote
56	156	11.3	638	~	T05606	protein kinase hom
27	155.5	11.2	942	-1	JQ1674	protein kinase TMK
28	155	11.2	729	~	F86308	Similar to disease
29	154.5	11.2	1143	N	T10636	hypothetical prote

AF0169 probable exported protein YPO1388 [imported] - Yersinia pestis (strain C092) C;Species: Yersinia pestis C;Species: Versinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C;Accession: AF0169

RESULT 2

hypothetical prote	probable disease r	probable receptor-	protein TIN15.9 [i	probable receptor	probable receptor-	probable disease r	probable protein k	hypothetical prote	receptor protein k	leucine-rich repea	probable receptor-	protein kinase Xa2	sericin MG-2 - gre	probable receptor	probable receptor-
T02361	T05257	B84852	G96524	A96557	H84632	T00971	F96557	F85343	T50851	T07079	B84782	T04313	C61615	E96631	B84659
				۰.	٠.										
0	~	7	N	• •	.,	~	N	~	N	7	N	N	~	7	N
720 2	668 2	646 2	655 2	838	980	480 2	693 2	863 2	981 2	221 2	672 2	813 2	286 2	645 2	976 2
				11.0 838 2											
11.1	11.0	11.0	11.0		11.0	10.9	10.9		10.9	10.9	10.9	10.9	10.8	10.8	10.8

ALIGNMENTS

THISHO	
D84434	[6.44.4.4.7]
C; Spec	probable receptor-like procein kinase (imporced) - Arabidopsis chailana C;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Ebh-2001 Hacamence revision 02-Eph-2001 Heart change 02-Eph-2001
C, Back	C. Gert. D. C.
R;Lin, M.; Ko	R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss,	euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Maring AC. 251-750 1909
A, Titl	Alitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Kere A; Acce	A;Accesion: D84434
A, Stat	A,Status: preliminary
A; MOLE	AfMOLECULE TYPE: UMA A.Residues: 1-1008 «STO»
A; Cros	A;Cross-references: GB:AE002093; NID:g6598459; PIDN:AAC78507.2; GSPDB:GN00139
C,Genetics:	C.Genetics:
A; Map	Ajene: Arguzzo AjMap position: 2
Quez	13.8%;
Matc	best Local Similarity 27.5%; Fred. No. 3e-Ub; Matches 68; Conservative 45; Mismatches 93; Indels 41; Gaps 12;
ò	9 CMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW 64
QQ	7 CVIVIFLTELLCFFYSSESQTTSRCHPHDLEALRDFIAHLEPRPDGWINSS-SSTDCCNW 65
à	65 EGVGCET-ASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
QQ	66 TGITCNSNNTGRVIRLELGNKKLSGKLSESLGKLDEIRVLNLSRNFIKDSIPLSI-FNLK 124
ζ	124 SLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNV 170
q	125 NLQTLDLSSNDLS-GGIPTSINLPALQSFDLSSNKFNGSLPSHICHNSTQIRVVKLAVNY 183
λο ·	171 VSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGN 225
Ωp	184 FAGNFTSGFGKCVLLEHLCLGMNDLTGNIPEDLFHLKRLNILGIQ 228
ò	226 DNNVSGS 232
QQ	: : 229 ENRLSGS 235

R. Parkhill, J. J. Wren, B. W.; Thomson, N. R.; Tithall, R. W.; Holden, M.T.G.; Prentice, M. B. B. Parkhill, J. J.; Wren, B. W.; Thomson, N. R.; Tithall, R. W.; Holden, M.T.G.; Prentice, M. B.	0y 144 SSRKILDEERWIJSGTNNSVOGGSN
A, Experimental source: cultivar Columbia, BAC clone F18A5 C, Genetics: A, Introns: 216/1; 541/1 A, Note: F18A5, 210	
13.4%; Score 186; DB 2; Length 645; arity 22.1%; Pred. No. 3.8e-06; onservative 46; Mismatches 115; Indels 128; VFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAM	Db 188 ESTELYRLALSFNSLSGPLPVSVARSYTLTFLDLQHNNLSGSIPDFFVNGSHPLKTLNLD 247 QY 199 NTVVGSNHVVSGTKHIVTDNNNVVSGPSFHTVSGEHNTVSGS 246 :
Db 67 CCSWDGISCDPRTGKVVELDLANSFLNGPLRYDSSLFRLQHLHNLDLGSNNFSGILPDSI 126 Oy 95 GELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV 143 : :	RESULT 5 G84524 probable disease resistance protein [imported] - Arabidopsis thaliana probable disease resistance protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

m

87

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Wed May

Accession: G84524

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Claccession: B8640

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudnes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; U.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1.590 <STO>
A;Cross-references: UNIPROT:Q9C867; GB:AE005172; NID:g11054670; PIDN:AAG27890.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all0406 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIIPSSIGELDHLRYLDLSGNSLVGEVPKS------LQIRLKSLTTDSQSLGMGSIN 138
                                                                                                                                                                                                          71 GEIPPSLGTLSHLTFLDLSENKLVGQVPSSIGNLTKLMYLRLSINHLSGKS-SVSFANLT 129
                                                                                                                                                                                                                                                                               139 MLLHVSSRRTLDEEPNTI---SGTNNSVGSGSNNVVSGNDNTVVS------GNNN 184
                                                                                                                                                                                                                                                                                                                                                     130 KLIQLDIREN-DFEPELIPDMSRFHNLEGFGGGNFFGPFPTSLFTIPSLRWVNLRDSNNN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 BVPKSL-----QIRLKS-LTTDSQSLGMGSINMLLHVSSRRTLDEBPNTISG----- 158
                                                              11 SWNKSSDCCSWESVTCDAKYGQVISLYLLGVNLNNTLKPNSGLFKLQYLQNLTLRYCNLY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 MKSCCSWLLLISLLCSLSNESQ------AISPDGEALLSFRNAVTRSDSFIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 -W--SGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AIPTALGNCTALBEIHLQSNYFIGPIPAEMGDLPGL-----QKLDMSSNTLSGPIPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TINISVGSGSINIVVSGN--DNTVVSGNINHVSGSNITVVTGSDNTVVGSNHVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 GQLKKLSNPNV---SNNFLVGQIPSDGVLSG------PSKNSFIGNLNLCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 FTGHIDFGNSSLSSRLSYLSLADNNFDGPIPESISKFLNIVJLDLRNNSFSGPFPT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5. MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                           ---HVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVV--SGNDNNVSGSFHT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 - KHV----- DVVCQDDSG-NPSSHSQSGQNQKKNSGKLLISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 12.5%; Score 173.5; DB 2; Local Similarity 24.7%; Pred. No. 2.8e-05; nes 70; Conservative 44; Mismatches 90;
       AWSGAS-CCSWEGVGCETASGRVVALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B86440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
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Best Local S:
Matches 70
   55
                                                                                                                                           88
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C84633
C966133
C566168: Arabidopsis thaliana (mouse-ear cress)
C566168: Arabidopsis thaliana (mouse-ear cress)
C5676168: Arabidopsis thaliana (mouse-ear cress)
C5767618: Arabidopsis thaliana (mouse-ear cress)
C5767619: Arabidopsis thaliana (mouse-ear cress)
C5777619: Arabi
Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; S. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. uss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q9ZUK3; GB:AE002093; NID:g4115363; PIDN:AAD03365.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9ZUH7; GB:AE002093; NID:g4115376; PIDN:AAD03377.1; GSPDB:GN
                                                              euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Very Nature 402, 761-768, 1999
Aritile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AAWSGAS-CCSWEGVGCETASGRVVAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 179.5; DB 2
Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%;
21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Conservative
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Best Local Similarity
Matches 63; Conserv
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Best Local Similarity
Matches 81; Conserv
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A; Residues: 1-983 <STO>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-743 <STO>
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A;Gene: At2g24160
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A, Map position: 2
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Gaps

22 51 165

Db 138 SALDQLLVLDLSYNSFKGELPLQQSFGNGSNGIFPICTVDLSSNLLEGEILSSS 191 Oy 183 NNHVSGSNNTVYTGSDNTVVGS 204 Db 192 VPLQGAFNLTSFNVSNNSFTGS 213 RESULT 10 C96519 Probable disease resistance protein, 3954-7013 [imported] - Arabidopsis thaliana (woise-ear cress) C,5pecies: Arabidopsis thaliana R,7fheologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, ansen, N.F.; Hughes, B.; Huizar, L. R,7fheologis, A.; Ecker, J., J., J., J., J., J., L., S. X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marxiali, A; Authors: Hughes, B.; Huizar, L. R,7file Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Retence number: Ascillationary A; Rosidues: 1-1019 A; Ro	Query Match 12.1%; Score 168; DB 2; Length 1019; Best Local Sminarity 23.2%; Pred. No. 0.00014; Matches 84; Conservative 50; Mismatches 106; Indels 122; Gaps 14; Qy 9 CMLLVFLGFILGVAGATSWSCHHDLARGLAENLSGKGAVIRDAMSGASCCSWEGYG 68	C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: H84421 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C; Accession: ABI857 R; Kaneko, T.; Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, DNA Res 8, 205-213, 2001 DNA Res 8, 205-213, 2001 A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: ABI807; MUD:21595285; FMID:11759840 A; Retence number: ABI807; MUD:21595285; FMID:11759840 A; Retence number: ABI807; MUD:21595285; FMID:11759840 A; Retence number: ABI807 A; Retence number: AB	REGULT 9 GG5746 Dypothetical protein T9N14.20 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-aar cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: G95746 Cint. C.W.; thugs, M.K.; Comp. L.; Colly, Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; thugs, M.K.; Comp. L.; Colly, A.B.; Colly A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 C,A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Mithors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.W.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shin, P.; Southwick, A.W.; Sun, H.; Tallon, A;Mclession: G95746 A;Status: preliminary A;Molecule type: DNA A;Mcles and analysis of Chromosome 1 of the plant Arabidopsis. A;Mcles and analysis of Chromosome 1 of the plant Arabidopsis. A;Mccession: G95746 A;Generics: A;Mccession: G95746 A;Generics: A;Mccession: G95746 A;Generics: A;Map position: 1 Query Match Best Local Similarity 28.7%; Pred. No. 0.00014; Indels 41; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 41; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 41; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 77; Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 77; Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 77; Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 58; Conservative 29; Mismatches 74; Indels 74; Gaps 9; A;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Matches 75;Match	Qy 135 GSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN 182

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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: H84421
A; Accession: H84421
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-716 <STO>
A; Cross-references: UNIPROT:Q9ZU46; GB:AE002093; NID:g4262228; PIDN:AAD14521.1; GSPDB:GN
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A; Appendix S. Appen
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: B85440
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprint Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85440
A;Accession: B85440
A;Accession: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 164.5; DB 2 27.4%; Pred. No. 0.00017; iive 34; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
C;Superfamily: protein kinase homology
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Best Local Similarity
Matches 63; Conserv
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Best Local Similarity
Matches 63; Conserv
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A;Gene: AT4g37250
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A;Introns: 863/1; 1116/1
A;Note: F1C12.60; F18F4.240
C;Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I.; Mewes, H.W.; Mayer, K.F.X
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                                                                                                                                            hypothetical protein P18F4.240 - Arabidopais thaliana
N;Alternate names: hypothetical protein F1012.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T05322; T04898
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15408
A;Accession: T05322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 EGVGCE-TASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 SLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNN--SVGSGSNNVVSGNDNTVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLVFLGFILQVAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS--GASCCSW
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203 GYSLQYLMVSFNQISGEIPPEIGVNFPRNVTVDLSFNNLTG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1232 - EBEV-
A; Cross-references: UNIPROT: Q9SN91; EMBL: AL022224
A; Experimental source: cultivar Columbia; BAC clone F1C12
R; Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft,
submitted to the Protein Sequence Database, February 1998
A; Reference number: 215388
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A,Residues: 1-773 <ROU>
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A;Molecule type: DNA
A;Residues: 1-305 - GBBW>
A;Cross-references: EMBL:AL021637
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9, 2005, 20:22:59
          A;Gene: F1913.16; At2g34930
A;Map position: 2
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Job time : 18 secs
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A;Cross-references: UNIPROT:022178; EMBL:AC002391; NID:g2642427; PID:g2642433
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rouneley, S.D.; Bhaito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; WanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Ayature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 LGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL----QIRLKSLTTDSQS----LGMGSI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNTVVGSNHVVSGT---KHIVTDNNNVVSGNDNNVSGSFHTVSG----EHNTVSGSNNTVS 251
                                                                                                                                                                                                                                                                                                                                                            Residues: 1-773 <STO>
Cross-references: GB:AE002093; NID:g2642433; PIDN:AAB87101.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 SWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 HNL-----QTLNLSDNIFTGKLPA-----NLASLGSLTEVSLKNNYFSGEFPGGGWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%; Score 162; DB 2; 27.3%; Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: At2g23300; T20D16.7
A,Map position: 2
A,Introns: 545/1
C,Superfamily: protein kinase homology
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Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                  Status: preliminary
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                                                                                                                                                                                                                                                                       Accession: A84623
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                                                                                                                                                                                                                                                                                                                                                                                                                                        189 LSSLSSSLKYLNMGYVNLSGAGETWLQDFSRISALKELHLFNSE-LKNLPPTLSSSADLK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 LLEVLDLSENSLNSPIPNWLFGLTNLRKLFLRWDFLQGSIPTGFKNLKLLETLDLSNNLA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 VTGSDNTVVG-----DNNVSGTKHIVTDNNNVVSGN-----DNNVSGSFHT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                               14 LILILLKNINYGSAASPKCISTERQALLTFRAALTDLSSR----LFSWSGPDCCNWPG
                                                                                                                                                                                                                                                                                                                                                                                          -LHVSSRRTLDEEPNTISG----
                                                                                                10 MLLVFLGFILQVAGATSWSCHHDDLHAL---RGLAENLSGKGAVRLRAAWSGASCCSWEG
                                                     Gaps
                                                  Indels 143;
  Length 905;
; Score 161.5; DB 2;
; Pred. No. 0.00037;
45; Mismatches 105;
                                                                                                                                                                                           67 VGCETASGRVVA--LRLP-----KRG--LGGI---
                                                                                                                                                                                                                                                                                            90 IPSSIGELDHLRYLDLSGNSLVGEVPKSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TINNSVGSGSNNVVSGNDN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLGSLRNLQTLDLSSNSFTGS 388
                                                                                                                                                                                                                                                                                                                                                                                       122 LKSLTTDSQSLGMGSINML-
11.7%;
23.1%;
Query Match 11.7%
Best Local Similarity 23.1%
Matches 88; Conservative
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TYPE: PRT
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Sequence 5, Appli
Sequence 5, Appli
Sequence 890, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 764, App
Sequence 902, App
Sequence 902, App
Sequence 80, Appl
Sequence 80, Appl
Sequence 7, Appli
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897, App
911, App
2676, Ap
953, App
                                                         9, 2005, 20:15:44 ; Search time 43 Seconds (without alignments) 463.519 Million cell updates/sec
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1 MPEYWAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-101-464A-902

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US-09-952-267B-7

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US-09-345-473E-15
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Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                   13, Appl
3401, Ap
3401, Ap
72, Appl
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932, Appl
11, Appl
772, Appl
773, Appl
75, Appl
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Sequence 9, Application US/09336447A

Setent No. 6310190

GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABL, CHRISTOPH

APPLICANT: ABL, CODE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
ITILE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILLE REFREENCE: AMCY:024

CURRENT APPLICATION UNBER: US/09/336,447A

CURRENT PILING DATE: 1999-06-21

NUMBER OP SEQ ID NOS: 98
                           Sequence 13, Sequence 13, Sequence 13, Sequence 79, Sequence 72, Sequence 72, Sequence 1, Ap Sequence 75, A Sequence 70, A Seq
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTIOES AMOUNT AND USPAL ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMOY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 IVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
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                               US-09-336-447A-13
US-09-952-267B-13
US-09-540-236-3401
US-09-540-236-79
US-10-101-464A-72
US-10-101-464A-92
US-10-101-464A-932
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Patent No. 6753417
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Moraxella catarrhalis
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SEQ ID NO 9
LENGTH: 941
US-09-952-267B-9
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDEMBURG, ROSS A.
TILLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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APPLICANT: ABBL, CRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKENGNG, ROSS A.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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31.8%; Pred. No. 2.9e-08;
ive 20; Mismatches 49; Indels
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SEQ TWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 892
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
FERMON OF PRIOR OF PATENTIN VER. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
APPLICANT: HANBEN, ERIC J. APPLICANT: ABBI, CHRISTOPH APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5, Application US/09952267B
; Patent No. 6753417
; GENERAL INFORMATION:
                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-952-2678-9
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US-09-336-447A-5
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Best Local Similarity 31.8<sup>1</sup>
Matches 35; Conservative
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Best Local Similarity
Matches 39; Conserva
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US-09-336-447A-5
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                                                                                                                                            LENGTH: 941
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Sequence 890, Application US/10101464A
Patent No. 6768041
Batent No. 6768041
BAPELICANT: NFORMATION:
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFERENCE: 11000.1020c2
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                                                                                                                                                                                                                                                                                                Query Match 12.8%; Score 177; DB 4; Length 892; Best Local Similarity 31.8%; Pred. No. 2.9e-08; Matches 35; Conservative 20; Mismatches 49; Indels
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; Pred. No. 2.8e-08;
54; Mismatches 105;
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FRIOR APPLICATION NUMBER: 09/704,302
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PELING DATE: 1999-11-01
PRIOR PILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 890
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                   TYPE: PRT ORGANISM: Moraxella catarrhalis
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23.4%;
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Best Local Similarity 25...
Best Tocal 77; Conservative
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                                                                                                                                                                          LENGTH: 892
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NAME/KEY: VARIANT
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US-10-101-464A-893
US-09-952-267B-15
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                                               239 NCTSLTDLVISSNNLSGPIPSEFSGLVSLKFLFLDDNSISGSIPTSLVNCTSLFALKGSG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 TTDSQSLGMGSINMLLHVSS------RTTLDEEPNTIS-GTNNSVGSGSNNVV 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 LGNNATISGGRQNEASGDRSTVAGGEQNQAIGKYSTISGGRQNEASGDRSTVAGGEQNQA 303
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APPLICANT: HANSEN, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: PREDRIBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT PILING DATE: 2001-09-12
PRIOR FILING DATE: 1999-06-21
PRIOR PILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 IGKYSTVSGGYRNQATGKGSFAAGIDNKANADNAVALGNKOVTIEGENSVAIGSNNTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER.
APPLICANT: PREDENBUG.
APPLICANT: FREDENBUG, ROSS A.
TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERRNČE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.6%; Score 175; DB 3; Length 889; Best Local Similarity 27.1%; Pred. No. 4.5e-08; Matches 48; Conservative 25; Mismatches 66; Indels 38;
                     --TGSDNTVVGSNHV-----VSGTKHIVTDNNNV
                                                                                                                             299 NKLSGPIPSVMGLMKSISTIDLSNNSLTG 327
                                                                                                   227 NNVSGSFHTVSG---EHNTVSGSNNTVSG 252
                                                                                                                                                                                                    RESULT 6
US-09-336-447A-15
US-09-336-447A-15
Sequence 15, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09952267B
Patent No. 6753417
GENERAL INFORMATION:
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ORGANISM: Moraxella catarrhalis
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ORGANISM: Moraxella catarrhalis
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LENGTH: 889
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US-10-101-4064-893.

US-10-101-4064-893.

Sequence 893. Application US/10101464A

Patent No. 6768041

GENERAL INPORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Niewwenhuizen, Nicolaas

APPLICANT: Miewwenhuizen, Nicolaas

APPLICANT: Miewwenhuizen, Sollated from Plant Cells

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT FILING DATE: 2002-03-18

PRIOR PILING DATE: 2000-10-01

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-01

SOFTWARE: FABLECATION NUMBER: PCT/US00/00724

NUMBER OF SEQ ID NOS: 989

SOFTWARE: PASESEQ for Windows Version 4.0

TENDENT PARTING DATE: 100-01-11

NUMBER OF SEQ ID NOS: 989
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                                                                                                                                                             172 SGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTK--HIVTDNNNVVSGNDNNV 229
                                                                                                                                                                                                                                                                             63 SWEGVGCETASGRVVALRLPXRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ------NNNHVSGSNNTVVTG-----SDNTVVGSNHVVSGTKHIVTDNNNV 221
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                                                                                                                                                                                                                                                                                                                                                                                                                  304 IGKYSTVSGGYRNQATGKGSFAAGIDNKANADNAVALGNKNTIEGENSVAIGSNNTV 360
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22.7%; Pred. No. 5.2e-08;
tive 55; Mismatches 107; Indels 110; Gaps
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                                                                  38;
         Length 889;
                                                               25; Mismatches 66; Indels
12.6%; Score 175; DB 4; 27.1%; Pred. No. 4.5e-08;
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-101-464A-893
         Query Match 12.6%
Best Local Similarity 27.1%
Matches 48; Conservative
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Best Local Similarity 22.7%
Matches 80; Conservative
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ORGANISM: Pinus radiata
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TYPE: PRT
ORGANISM: Pinus radiata
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ORGANISM: Pinus radiata
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000-102002
253 SRLVRLETLLFDDNSISGSIPASISNCTSLQYLDISDNSLSGP------IPSEFSRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLD 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LSSNALSGRIPAEFGQLKALRILDLSNNALTGSIPTCIGNGGLNGTL-----DLDLSWN 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSGNSLVGEVPKSL----QIRLKSLTTDSQS-----LGMGSINMLLHVSSRRTLDEEPN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 TISG-------TINNSVGSGNNAVVSGNDNTVVSGNN--NHVSGSNNTVV- 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 MLLVFLGFIL----------------QVAGATSWSCHHD--DLHALRGLAE--NL 44
                                                                 VS-----GNDNNVSGSFHTVSGEHNTVS----GSNNTVSGSNHIVSGSNKVVT 265
                                                                                          DB 4; Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; Score 171.5; DB 4; 25.5%; Pred. No. 2.4e-08; tive 52; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 2002-03-18
PRIOR FILING DATE: 2002-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1099-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
STONDMER: FESTESE for Windows Version 4.0
SEQ ID NO 764
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                               Sequence 764, Application US/10101464A Patent No. 6768041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 GSNNTVSGSNHIVSGSNKVVT 265
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Best Local Similarity 25.5
Matches 82; Conservative
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ORGANISM: Pinus radiata
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Sequence 902, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas

RESULT 10 US-10-101-464A-902

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APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
FRIOR PELICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/104,302
PRIOR PLING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6359198
GENERAL INFORMATION:
BAPPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REPERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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STREET FARTER OF THE STREET FOR WINDOWS OF THE STREET FOR WINDOWS: 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 CNOSDVQALISFKQTVSSSSPIN----WEVNRSCCTWEGVTCGLLSLQOFSVTKLRLPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CHHDDLHALRGLAENLSGKGAVRLRAAWS-GASCCSWEGVGCETASGR----VVALRLPKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 170.5; DB 4; Length 386; ; Pred. No. 3.8e-08; 25; Mismatches 61; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEINSIRTFNISSNSFRGNVPQLGSAVNLTSFNVSNNSFTG 191
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Best Local Similarity 26.1%; Pred. No. ...
Marches 81; Conservative 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 LKSLTTDSQSLGMGSI----NM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.3%
Matches 52; Conservative
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ch 12.3%; Score 170; DB 4; 1 Similarity 30.6%; Pred. No. 8.3e-08; 38; Conservative 24; Mismatches 50
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                                     Sequence 7, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION: APPLICANT: HANSEN, ERIC J. APPLICANT: AEBI, CHRISTOPH APPLICANT: COPE, LEGLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 7
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Best Local Similarity
Matches 38; Conservat
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US-09-952-267B-7
RESULT 13
US-09-336-447A-7
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Fatent No. 6768041

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
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                                                                                                                            -----SDNTVVGSNHVV---SGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                   -----GGNSNK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 -SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIR 121
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TQNLPQSFSSLSSLSVLYLQNNQL-AGSVNVLANLPLTDLNIENNRFSGWVPNAWRSNQN 236
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119 LQELNLASNGLS-GTIPYSISNWTGLTDLKLSHNQLSGQIQDIFGQLSSLSTLDLSFNTL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSTLDLSFNTL 177
                                                                 9 CMLLVFLGFILQVA---GATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCC-
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                                                                                                                                                    237 FKYSSGNSFATGPAPPPPPYTPPPPSNNRPPKSSNVVPSSGGSK-
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PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PELING DATE: 1999-11-01
PRIOR PELING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                          189 ----SNNTVVTG-
                                           157 SGT-----
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US-10-101-464A-80
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SEQ ID NO 80
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154 NTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKH 213
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TILE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS FILE REPERBUCE: AMCY:024
CURRENT FALLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION UNDERR: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.3%; Score 170; DB 3; Length 624; Best Local Similarity 30.6%; Pred. No. 8.3e-08; Matches 38; Conservative 24; Mismatches 50; Indels 1
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WESULT 15
US-10-101-464A-732

Sequence 732, Application US/10101464A

Fatent No. 6768041

Sequence 732, Application US/10101464A

Fatent No. 6768041

Settle No. 6768041

APPLICANT: Strabala, Timothy

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cells

FILE REFERENCE: 11000.102022

CURRENT APPLICATION NUMBER: US/10/101,464A

FILE REPLAYION NUMBER: 09/704,302

FRIOR APPLICATION NUMBER: 09/704,302

FRIOR PILING DATE: 1999-01-12

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR FILING DATE: 1999-11-01

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR FILING DATE: 1999-11-01

FRIOR APPLICATION NUMBER: 60/162,866

FRIOR FILING DATE: 1999-11-01

FRIOR APPLICATION NUMBER: 09/200/00724

FRIOR APPLICATION NUMBER: 2000-01-11

FRIOR
214 IVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS-----GSNNTVSGSNHIVSG---SN 261
                                                                       164 QANTDNAVALGKNNTINGNNSAAIGSENTVNENQKNVFILGSNTTNAQSGSVILGHETSG 223
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US-10-101-464A-732
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Search completed: May 9, 2005, 20:22:40 Job time: 49 secs

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May 9, 2005, 20:21:56; Search time 138 Seconds (without alignments) 645.441 Million cell updates/sec
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1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267
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(SGNZ_6/ptodata/2/pubpaa/US07_PUBCOMB. PDP: *

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(SGNZ_6/ptodata/2/pubpaa/US09_PUBGOMB. PDP: *

(SGNZ_6/ptodata/2/pubpaa/US108_PUBGOMB. PDP: *

(SGNZ_6/ptodata/2/pubpaa/US1108_PUBGOMB. PDP: *

(SGNZ_6/ptodata/2/pubpaa/US108_PUBGOMB. PDP: *

(SGNZ_6/ptodata/2/pubpaa/
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
                                          Copyright
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2014161
2018
2018
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	% Query Match	% Query Match Length DB	DB	ΩI	Description	
1	262	18.9	1010	16	US-10-437-963-180288	Sequence 180288	180288,
7	206.5	14.9	1039	16	US-10-437-963-166082	Sequence	166082,
٣	204	14.7	1021	15	US-10-443-101-2	Sequence	2, Appli
4	198	14.3	264	16	US-10-437-963-148813	Sequence	148813,
ß	197	14.2	961	16	US-10-437-963-172660	Sequence	172660,
9	194	14.0	917	16	US-10-437-963-115627	Sequence	115627,
7	194	14.0	1164	16	US-10-437-963-192784	Sequence	192784,
89	192.5	13.9	838	16	US-10-437-963-169754	Sequence	169754,
Ø	192	13.9	1060	16	US-10-437-963-153194	Sequence	153194,
10	190	13.7	1044	16	US-10-437-963-162505	Sequence	162505,
11	188.5	13.6	1011	16	US-10-437-963-172329	Sequence	172329,
12	188.5	13.6	1078	16	US-10-437-963-123119	Sequence	123119,
13	186	13.4	278	15	US-10-424-599-267766	Sequence	267766,

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Gaps

34;

64 67

7 KCCML-LVFLGFILQVAGATSWSCHHDDLHALRGLAENLS-GKGAVRLRAAWSGASCCSW

18.9%; Score 262; DB 16; Length 1010; 40.1%; Pred. No. 1e-13; tive 19; Mismatches 53; Indels 34

Query Match
Best Local Similarity 40.1%
Matches 71; Conservative

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65 EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124

186 13.4 676 16 US-10-437-963- 183.5 13.2 13.3 16 US-10-437-963- 183.5 13.2 13.3 16 US-10-437-963- 183.5 13.2 13.3 16 US-10-437-963- 182 13.1 13.1 16 US-10-437-963- 181 13.1 13.1 16 US-10-437-963- 181 13.1 13.1 16 US-10-437-963- 181 13.1 10 US-10-38-556- 181 13.1 10 US-10-38-556- 180 13.0 10.0 US-10-437-963- 180 13.0 10.0 US-10-437-963- 180 13.0 10.0 US-10-437-963- 178 12.9 516 15 US-10-437-963- 178 12.9 516 15 US-10-437-963- 178 12.9 151 16 US-10-437-963- 178 12.9 151 16 US-10-437-963- 178 12.9 151 16 US-10-437-963- 177 12.8 892 10 US-03-95-556- 177 12.8 892 10 US-03-95-556- 177 12.8 892 10 US-10-437-963- 176.5 12.7 804 17 US-10-437-963- 177 12.8 892 10 US-10-437-963- 177 12.8 892 10 US-10-437-963- 175 12.6 10.0 16 US-10-437-963- 174 12.6 883 14 US-10-10-464, 174.5 12.6 10.0 16 US-10-437-963- 175 12.6 10.0 16 US-10-43	Sequence 153306, 92786 Sequence 13619, 50876 Sequence 136619, 50876 Sequence 136619, 50876 Sequence 150876, 19802 Sequence 10913, 625 Sequence 102913, 625 Sequence 10291, 625 Sequence 10291, 625 Sequence 10291, 627 Sequence 10291, 6281 Sequence 10291, 6281 Sequence 10291, 6282 Sequence 10291, 6282 Sequence 170316, 6282 Sequence 170316, 6282 Sequence 170316, 6282 Sequence 114827, 62882 Sequence 114827, 62882 Sequence 138726, 62892 Sequence 138726, 62892 Sequence 138726, 62892 Sequence 138726, 67059 Sequence 167059, 67059 Sequence 167059, 67059 Sequence 18888, 67059 Sequence 18888, 67059 Sequence 1893, Appl	es and Other Molecules Associated With for Plant Improvement
14 186 13.4 676 16 15 185 13.4 1012 16 16 183.5 13.2 1380 16 18 183.5 13.2 1380 16 19 182 13.1 13.1 16 21 181 13.1 1653 15 22 181 13.1 1653 15 23 181 13.1 1653 15 24 180.5 13.0 675 16 25 180 13.0 1036 16 27 179 12.9 516 15 29 178 12.9 153 15 29 178 12.9 151 16 31 177.5 12.8 892 10 34 176.5 12.7 804 14 34 176.5 12.7 862 15 38 175.5 12.6 889 10 40 175 12.6 889 10 41 174.5 12.6 889 10 42 174.5 12.6 889 10 43 174.5 12.6 889 10 44 174.5 12.6 889 10 45 174.5 12.6 889 10 46 175.5 12.7 804 14 47 174.5 12.6 889 10 48 174.5 12.6 889 10 49 175.5 12.7 804 14 41 174.5 12.6 889 10 42 174.5 12.6 889 10 43 174.5 12.6 889 10 44 174.5 12.6 889 10 45 174.5 12.6 889 10 46 175.5 12.7 1036 16 47 174.5 12.6 889 10 48 174.5 12.6 889 10 49 175.5 12.7 1036 16 48 174.5 12.6 889 10 48 174.5 12.6 889 10 48 174.5 12.6 889 10 49 175.5 12.7 1036 16 48 174.5 12.6 889 10 49 175.5 12.6 889 10 40 175.5 12.6 889 10 41 174.5 12.6 889 10 42 174.5 12.6 889 10 43 174.5 12.6 889 10 44 174.5 12.6 889 10 45 174.5 12.6 889 10 46 175.5 12.7 1036 16 47 174.5 12.6 889 10 48 174.5 12.6 1000 16 48 174.5 12.6 10	10-437-963-1 10-437-963-1	ENTS olecules ereof for 63
14 186 13.4 15 185 13.4 16 183.5 13.2 19 183.5 13.2 19 183.5 13.1 22 13.1 22 13.1 23 13.1 24 180.5 25 180 13.0 26 180 13.0 27 179 12.9 29 178 12.9 30 178 12.9 31 177.5 12.8 33 177.5 12.8 34 176.5 12.7 38 17.5 12.8 31 177.5 12.8 33 177.5 12.8 34 176.5 12.7 38 176.5 12.7 38 176.5 12.7 38 176.5 12.7 38 176.5 12.7 38 176.5 12.7 39 177.5 12.8 31 177.5 12.8 31 177.5 12.8 32 177.5 12.8 34 176.5 12.7 38 176.5 12.7 38 176.5 12.7 39 177.5 12.8 34 174.5 12.6 42 174.5 12.6 44 174.5 12.6 45 174.5 12.6 47 174.5 12.6 48 174.5 12.6 48 174.5 12.6 48 174.5 12.6 49 175.1 12.8 48 174.5 12.6 49 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 41 174.5 12.6 42 174.5 12.6 43 174.5 12.8 44 174.5 12.6 45 17.7 47 17.5 12.8 48 177.5 12.8 49 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 40 177.5 12.8 41 174.5 12.6 42 174.5 12.6 44 174.5 12.6 45 176.5 47 176.5 48 177.5 48 178 178 178 178 178 178 178 178 178 17		nation Ug 123343A. 123343A. 123343A. Andrey Brad Cee Nucle 11ants an 153221)B MBER: Ug 153221)B MBER: Ug
SULT 1 14 188 183: 16 183: 18 183: 18 183: 19 183: 20 183: 21 183: 22 186: 24 180: 25 186: 26 180: 27 177: 33 177: 33 177: 34 177: 38 176: 38 176: 39 177: 39 177: 39 177: 39 177: 39 177: 39 177: 39 177: 39 177: 30 177: 31 177: 32 177: 34 177: 36 176: 37 177: 38 176: 39 177: 39 177: 39 177: 30 177: 31 177: 32 177: 31 177: 32 177: 33 176: 34 177: 36 176: 37 177: 38 176: 38 177: 38 176: 39 177: 31 177: 31 177: 32 177: 33 176: 36 176: 37 177: 38	4.4.2.2.2.1.1.1.1.0.0.0.0.0.0.0.0.0.0.0.0.0	180288 Applic 0288, Applic 02804(2004(2004(2004(2004(2004(2004(2004
88 80 80 80 80 80 80 80 80 80 80 80 80 8		RESULT 1 US-10-437-963 Sequence 18 PUBLICANT: APPLICANT: APPLICANT

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.6%
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
               SEQ ID NOS: 5
PatentIn version
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                                                                                                                                                                TYPE: PRT
ORGANISM: Daucus carota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
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Best Local Similarity
Matches 70; Conserv
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               NUMBER OF SEQ ID
                                                                                                                         LENGTH: 1021
                                                                                                                                                                                                                       ; US-10-443-101-2
                                                   SOFTWARE: 1
SEQ ID NO 2
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 -SINIVIVSGN------DNTVVSGNNNHVSGSNNTVVTGSDN--TVVGSNHVVSG---T 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LTTDSOSLGMGSINMLLHVSSRRTLDEEPNTISGT-----NNSVGSGSNNVVSG 173
                                                                                                                                                                        -----GGISALLAAVSLRTANLSSNLLNDTLLDLAALPHLSAFNASNNSLSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 1039;
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Sequence 2, Application US/10443101

Sequence 2, Application US/10443101

Sequence 2, Application No. US20040096941A1

GENERAL INFORMATION:

APPLICANT: MATSUBAYASHI, YOSHIKATSU

TILE OF INVENTION: RECEPTOR FOR FLANT CELL GROWTH FACTOR

FILE REFERENCE: 238013USO

CURRENT APPLICATION NUMBER: US/10/443,101

CURRENT FILING DATE: 2003-05-22

PRIOR APPLICATION NUMBER: 19P 2002-335572

PRIOR FILING DATE: 2002-11-19
212 KHIVTDNNNVVSGNDNNVSG-----SFHTVSGEHNTVSGS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 SLGMLPNLYELSLGFNNLSGPIPTSIWNISSLRALSVOGNMLSGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.9%; Score 206.5; DB 16; Length Best Local Similarity 29.1%; Pred. No. 6.6e-09; Matches 83; Conservative 52; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_64826C.1.pep
US-10-437-963-166082
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166082, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                                     -10-437-963-166082
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                                               68
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APPLICANT:
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                               106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 FSSNCCDWVGISCKSSVSLGLDDVNESGRVVELELGRRKLSGKLSESVAKLDQLKVLNLT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 GNSLVGEVPKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISG---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 HNSLSGSIAASLINLSNLEVLDLSSNDFS---GLFPSLINLPSLRVLNVYENSFHGLIPA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 SLCNNLPRIREIDLAMNYFDGSIPVGIGNCSSVEYLGLASNNLSGSIPQELFQLSNLSVL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 TGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTV-----SGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 ALQNNRLSGA----LSSKLGKLSNLGRLDISSNKFSGKIPDVFLELNKLWYFSAQSNLFN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
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                                                                                                                                                                                                                                                                                                                                                           8 VILILVGFCVQIVVVNSQNLTCNSNDLKALEGFMRGLESSIDG------WKWNESSS
                                                                                                                                                                                                                                                                                                                                                                                                                                               58 -GASCCSWEGVGCETA-----SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLS
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                                                                                                                                                                                                                                                                                                                         10 MLLVFLGFILQ--VAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS----
                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                      Length 1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.3%; Score 198; DB 16; Length 264; 27.6%; Pred. No. 6.2e-09; ive 42; Mismatches 116; Indels 26
                                                                                                                                                                                                                                                                 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 --TINN------SVGSGSNINVVSGNDNTV--VSGNNNHVSG-
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                                                                                                                                                                                                      ; Score 204; DB 15;
; Pred. No. 1.1e-08;
56; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NNTVSGSNHI 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 148813, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Boukharov, Andrey A.
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Sequence 192784, Application US/10437963
; Sequence 192784, Application US/10437963
; Publication No. US2040123343A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Shoukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Butten Depart Control of the Control of th
                                                                                                                            APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 19-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 115627
LENGTH: 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 ---SVPGGFPRSSSLRVLDLSRNLLEGEIPADVGEAGLLKSLDVGHNLFTGELPESLRGL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SNNVVSGNDNTVVS-----GNNNHVSGSNNTV--V 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 TGSDNTVVGSNHV------VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 194; DB 16; Length 9 26.3%; Pred. No. 6.8e-08; tive 43; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_19205C.1.pep
US-10-437-963-115627
                                        Kovalic, David K
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.3*
Matches 81; Conservative
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ORGANISM: Oryza sativa
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289 LSGNALTG 296
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
61 WEGIAC-GSNGTVTELSLPSMALEGPISVSIANLTGIRRLDLSYNSLSGELPPEL---1S 116
                                                                                                    124 SLTIDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSG---SNNVVSGNDNTVVS 180
                                                                                                                                                181 GNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTD-NNNVVSGNDNNVSGSFHTVSGE 239
                                                                                                                                                                                                                                                                            67 VGCETASGRVVALRIPKRGLGGIIPSSIGELDHIRYLDLSGN-SLVGEVPKSLQIRLKSL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 TTLILLGCSFTGDIPEQIGALRQLTFLALNSNKFTGGIPPTLGLLSKLFWLDLSDNQLSG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70775C.1.pep
US-10-437-963-172660
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Best Local Similarity 29.5%; Pred. No. 4e-08;
Matches 82; Conservative 38; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 172660, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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US-10-437-963-115627
; Sequence 115627
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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221 -RVLKASNNEINGS 233
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ORGANISM: Oryza sativa
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Sequence 153194, Application US/10437963

Sequence 153194, Application US/10437963

Sequence 153194, Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: Andrey A.

APPLICANT: Boukharov, Stand Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 153194

LENGTH: 1060
      127 IDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNN-----VVSGNDNTVVS 180
                                              346 ----IFSGSIVV-----LDVSFNRLGGELQEVDSSSSDWPLQVLNISSNLFTGAF 391
                                                                                                                                                                             392 PSTTWEKMSNLVAINASNNSFTGHIPSSFCISSLSFAALDLCYNQFSGEIPAGIGKCSAL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 KSLTTDSQSL----GMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VSGNN--NHVSGSNNTVVTGSDNTVVGSNHVVSG------TKHIVTDNNNVVSGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 VSGNSFAGHVDAAALCGASPGLRTLRLSMNGFSGDFPVGFGQCRSLVELSLDGNAIAGAL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VLVLLLLLVLKNGAAQSRCSSGDLAALRGFSAGLDGGVDGWPAGVGNASSSSTSDGGDCC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLVFLGFILQVAGATSWSCHHDDLHALRGLAENL-----SGKGAVRLRAAWSGASCC
                                                                                                                                                                                                                                                                                    452 RMLKAGHNNISGALPDDLFHATSLEY--LSFPNNGLQGTIKLVIKLSNLVFLD 502
                                                                                                                                                                                                                                           225 ----NDNNVSGS----FHTVSGEHNTVSGSNNTVSGS-NHIVSGSNKVVTD 266
                                                                                                                         181 GNNNHVSGSNNTVVTGSDNTVVG---SNHVVSGTKHIVTD-----NNNVVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.9%; Score 192; DB 16; Length 1 Best Local Similarity 27.5%; Pred. No. 1.2e-07; Matches 72; Conservative 44; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_53170C.1.pep
US-10-437-963-153194
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; Sequence 162505, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zovalic, David K.
; APPLICANT: Zovulic, Thua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDDVFGLTSLOVLSLHTNSLSG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
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; Sequence 169754, Application US/10437963
; Sequence 169754, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yinua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
    APPLICANT: Burbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: DATE: 2003-05-14
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169754
                                                                                                                                                                                                                                                                                                                                                                                       65 EGVGCETASGRVVALRLPKRGLG----GIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                            621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 IRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNT-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNTVVGSNHVVSG--TKHIVTD-NNNVVSGNDNNVSG-----SFHTVSGEHN----- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 LGFGKPSTVTLLEYVHISSFSLPEERLTLLRFLAE-LSPPHDNGLAASWRNRTDCCTWEG 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LGF-----ILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEG 66
                                                                                                                                                                                                                                                                                                             -----GFPAIE-VVNVSSNGFTGPHPAFPGAPNLTVLDITGNAFSGGINVTA
                                                                                                                                                                                                                                                                 8 CCMLLVFLG---FILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NVSGNINIHVSGS------NINTVTGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 LCASPVKVLRFSANAFSGDVPAGFGQCKLLNDLFLDGNGLTGSLPKDLYTIPELRWLSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 194; DB 16; Length 1164; 25.7%; Pred. No. 9.2e-08; tive 38; Mismatches 111; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 838;
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13.9%; Score 192.5; DB 16; Length
Best Local Similarity 28.3%; Pred. No. 8.1e-08;
Matches 83; Conservative 37; Mismatches 106; Indels
                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_88983C.1.pep
US-10-437-963-192784
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US-10-437-963-169754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 ----TVSGSNNTVSGS------NHIVSGSN 261
                                                                                                                                           Query Match
Best Local Similarity 25.7%
Matches 87; Conservative
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
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APPLICANT: Li, Ping;
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 123119
LENGTH.
12;
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                                                                                                                                                                                                                                                                            171 VSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVS 230
                                                                                                                                                                                                                                                                                                                                                                                 170 --SNLTTLV----KPIIETN--PIDGKDLSWMGN---LTSLTHFVLEGNRFT----GNIP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 VGCGGAGDGDGAVTRLSLPGRGFNGTISPSIGNLTGLTHLNLSGNSLAGQFPEVLFSLPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 VIVVDVSYNCLSGELPSVATGAAARGGLSLE-VLDVSSNLLAGQFPSAIWEHTPRLVSLN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||| :| :| :| :| || :| 187 ASNNSFHGSIPSLCVSCPALAVLDLSVNVLSG----VISPGFGNCSQLRVLSAGRNN--L 240
                                                                                                                                                61 ----CCSWEGVGCETA--SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEV 114
                                                                                                                                                                                              58 PAPVICOWTGVSCNNRRHPGRVTTLRLSGAGLVGTISPQLGNLTHLRVLDLSANSLDGDI 117
                                                                                                                                                                                                                                             115 PKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GTNNISVGSG-----SGSNNTVVSGNDNTVVS----GNNNHV----SGSNNTVV 194
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                                                   9
                                                                                               57
                                                                             4 MISELTHALLLOTVTSQTINGDDLSAL----LSFKSLIRDDPREVMSSWDTAGNGTNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LVFLGFILQVAGAT----SWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGA-SCCSWEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 VGCETA---SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPK----
                                                 11 LLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVR----LRAAWSGAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Gaps
  49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 1078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
  88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Clone ID: PAT_MRT4530_25984C.1.pep
US-10-437-963-123119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(1078)
OTHER INFORMATION: unsure at all Xaa locations
  32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 123119, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La ROBa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
  74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza Bativa
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US-10-437-963-123119
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NAME/KEY: unsure
LOCATION: (1)..(1
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  Matches
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                                                                                          APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162505
LENGTH: 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172329
LENGTH: 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GASC -- CSWEGVGCETASG -- RVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 VPKSL----QIRLKSLTTDSQSLGMGSİNMLL-HVSSRRTLDEEPNTISGTNNSVGSG-- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 -----SINIVVSGNDNT----VVSGNNNHVSGSNNTVVTGSDNTV-- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 PSLTQCTHLQQVVLCNNKLQGRIPTKFGMLHELKTLDLSNNALTGDIPPLLGSSPSFVYV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPEYMAKCCMLLVFLG-FILQVAGATSWSCHHD-DLHALRGLAENLSG-KGAVRLRAAWS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 -VGSNHVVSGTKHIVTDNNN--VVSGNDNNVSGSFHTV---SGEHNTVSGSNNTVSGS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 DLGGNQLTGGIPEFLANSSSLQVLSLKQNNLTGGIPPSLFNSSKLTTIYLNRNNLVGS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIRLFASCPKLIPLLAVPIPSSSLPLAISDDTDTDTRALLCFKSQISDPNGAL---SSWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.7%; Score 190; DB 16; Length 10
Best Local Similarity 26.5%; Pred. No. 1.8e-07;
Matches 79; Conservative 47; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70476C.1.pep
US-10-437-963-172329
                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: PAT_MRT4530_61590C.1.pep
US-10-437-963-162505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                              Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%;
30.5%;
                                                                        Barbazuk, Brad
     Cao, Yongwei
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
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US-10-437-963-172329
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ઠે 셤 ઠે 원 ð 셤 ò g ŝ 셤 32;

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APPLICANT: Boucharov, Andrey A.
APPLICANT: Boucharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 101513210/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 S--CCSWEGVGCETASGRVVALRLPKRGLGGIIP-SSIGELDHLRYLDLSGNSLVGEVPK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 SLQIRLKSLTTDSQSLGMGSINM---LLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 EL-LSLASLIGIHLQINAFSGALPPELARLRALQVLDLSFNGFNGTLPAALSNLTQLVAL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPEYMAKCCMLLVFLGFILQVAGATSWSCHHDDLHALR-GLAENLSGKGAVRLRAAWSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CCMLLVFLGFILQVAGATSWS--CHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 N-DNTVVSG-----NNNHVSGSNNTVVTGSDNTVVGSNHV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.4%; Score 185; DB 16; Length 1012; Best Local Similarity 25.6%; Pred. No. 4.6e-07; Matches 87; Conservative 35; Mismatches 116; Indels 102
                                                                                                                                                                                                                                                                                                            Length 676;
                                                                                                                                                                                                                                                                                                                                                            98; Indels
                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_53274C.1.pep
US-10-437-963-153306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT4530_88985C.1.pep
                                                                                                                                                                                                                                                                                                    13.4%; Score 186; DB 16;
30.4%; Pred. No. 2.3e-07;
tive 30; Mismatches 98;
                                                                                                                                                   LOCATION: (1)..(676)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-437-963-192786
; Sequence 192786, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 30.4%
                                               TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
                                                                                                 FEATURE: NAME/KEY: unsure
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SEQ ID NO 153306
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERROCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                        Sequence 267766, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A Rosa Thomas J
APPLICANT: A Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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| SRIPEDF-ANLKSLRNLYLQGNFFSGEVSDSVFALQNLVRLNLGNNNFSGEISPKFNSLT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 -----ASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPEYMAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSG-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKSARVKEAILLVFMFSLLSIA-----C--SDLASDRA------GLLLLRSAVGGRT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 RLATLYLERNNFTGSIPDLDAPPLDQFNVSFNSLTGSIPNRFSRLDRTAFLGNS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TINNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.4%; Score 186; DB 15; Length 278; Best Local Similarity 30.3%; Pred. No. 7.2e-08; Matches 71; Conservative 23; Mismatches 70; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83815C.1.pep
US-10-424-599-267766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(278)
OTHER INFORMATION: unsure at all Xaa locations
                  195 TGSDNTVVGSNHVVSGTKHIVTDNNNV 221
                                                          241 TGE---LPGELFDVKALQHLELPANOI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153306, Application US/10437963;
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Glycine max
                                                                                                                                                                   US-10-424-599-267766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 267766
LENGTH: 278
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120 IRLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNT-- 177

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: :::	VVSGNNMHVSGS197	168 LCASPVKVLRFSANAFSGDVPAGFGQCKLLNDLFLDGNGLTGSLPKDLYMMPALRKLSLQ 227	198 DNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHN 241	ENKLSGSLDDDLGNLTEITQIDLSYNMFNGNIPDVFGKLRSLESLNLASNQLNGTLPLSL 287	SB	SSCPWLRVVSLRNNSLSGEITIDCRLLTRLNNFDAGTNKL 327
122	178V	168 LCASPVKV	198 DNTVVGSNI	228 ENKLSGSL	242T	288 SSCPMLRV
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Search completed: May 9, 2005, 20:34:42 Job time : 144 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2005, 20:10:27 ; Search time 73 Seconds May Run on:

(without alignments)
1414.589 Million cell updates/sec

US-10-657-852A-15

1385 1 MPBYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* A_Geneseq_16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aab25515 Pinus rad Abu34968 Protein e Aaw68208 M. catarr Aab25518 Pinus rad Abb31206 Herbicida Aab2545 Pinus rad Aab2547 Pinus rad Aab2551 Pinus rad Aab2551 Pinus rad Aab2561 Pinus rad Aab2541 Pinus rad Aab2541 Pinus rad Aab6791 Pinus rad	
AAB25515 ABU34968 AAW68208 AAB25518 AAB25518 AAB25512 AAB2512 AAB2512 AAB2513 AAB25413 AAB25413 AAB35413 AAB31562 AD036979	AD132622 AAM42228 AAM42230 AAM42232 ABB92188 ADN72847
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176.5 176.5 175 173.5 171.5 170.5 170.5 170.1 170.5 168.5 166.5	165 165.5 165.5 165.5 165
0 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1 4 4 4 4 4 4 2 0 1 1 1 1 1 1 2 2

ALIGNMENTS

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/note=""Conserved leucine-rich repeats"
25. .26 /note="7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                     /note= "Conserved Cys pairs identified N-terminal of leucine-rich repeats of receptor-like kinases"
                                                                            Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout, litholytic, nephrotropic, cytostatic.
                                                               Perennial ryegrass antifreeze protein AFP2.
                                                                                                                               1. .23
/label= Signal_peptide
                                                                                                                      Location/Qualifiers
             ADM41473 standard, protein; 267 AA.
                                               (first entry)
                                                                                                       Lolium perenne.
                                               03-JUN-2004
                               ADM41473;
                                                                                                                       Key
Peptide
                                                                                                                                               Region
                                                                                                                                                                        Region
                                                                                                                                                                                       Region
RESULT 1
        ADM41473
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09-SEP-2003; 2003WO-NZ000199 WO2004022700-A2. 18-MAR-2004.

(GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.

09-SEP-2002; 2002US-0409557P

Hall C, Fish SA; Demmer J Shenk MA,

WPI; 2004-248453/23. N-PSDB; ADM41460. New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).

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Misc-difference
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ses 251;
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                                   The present sequence is that of AFP2, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymuclocitides can canding them ADM41458-ADN41483. The polymuclecitides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymuclecitides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymuclecitide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded CR NA corresponding to the polymuclecitide into the cells of the organism, antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by bloorystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and control and protect a plant from damage due to frost or freezing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPEYWAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fescue; cold tolerance; transgenic; plant; antigout;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1385; DB 8; Length 267; 100.0%; Pred. No. 5.4e-114; ive 0; Mismatches 0; Indels 0;
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/note= "Conserved leucine-rich repeats"
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/label= Signal_peptide
61. .72
/note= "Conserved Cys p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      litholytic; nephrotropic; cytostatic.
Claim 7; SEQ ID NO 16; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM41474 standard; protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tall fescue antifreeze protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schedonorus arundinaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegass and tall fescue)

cutifreeze proteins and the polymucleotides encoding them ADMA1458-

ADM41483. The polymucleotides were isolated from tissues taken at the polymucleotides were isolated from different parts of the plants. The polymucleotides can be used to modulate the cold to the plants. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by blocrystals associated with disorders such as gout and kindey stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient of the control of the control of the control of a protect a plant from damage due to
                                   154. .268
/note= "7-amino acid sequence repeat region identified in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Pred. No. 1.4e-105;
6; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fish SA;
/note= "Encoded by TAG
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                                                                                                               antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESIS RES & DEV CORP LTD (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall C,
                                                                                                                                                                                                                                                                                                                                             09-SEP-2003; 2003WO-NZ000199.
                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2002; 2002US-0409557P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-248453/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADM41461.
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(GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-248453/23
    frost or freezing.
                             Sequence 262 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004022700-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-C different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the vieblity of a molecular biology reagent, to debycout under the coll and the coll of the organism.
                                                                                                                                                                                                                                                                                                                                                                  /note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                                                                                  /note= "Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                 Antifreeze, fescue, cold tolerance, transgenic, plant, antigout,
litholytic, nephrotropic, cytostatic.
                                                                                                                                                                                                                                                                                                                               /note= "Conserved leucine-rich repeats" 147. .261
Fish SA;
                                                                                                                                                                                                                                                             1. .23
/label= Signal_peptide
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                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENESIS RES & DEV CORP LTD.
                                                                               ADM41481 standard; protein; 262 AA
                                                                                                                                                      Tall fescue antifreeze protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2003; 2003WO-NZ000199.
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                                                                                                                               (first entry)
                                                                                                                                                                                                                        Schedonorus arundinaceus.
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/note= "
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N-PSDB; ADM41468.
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              241
                                                                                                       ADM41481;
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                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                        182
                                                                                                                                                                                                                                                                                                                                                   242
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "7-amino acid sequence repeat region identified in
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                                                                                                           63
                                                                                                                                                                                                               64 WEGYGCETASGRYVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK
                                                                                                                                                                                                                                                                                                                     124 SLITDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN
                                                                                                        5 MAKCCMLLVPLGFILQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                                                                                                          1 MAKCIMILISFAFILISAAGTATATPCHRDDLRALRGFAENIGGGGALSLRAAWSGASCCD
                                                                                                                                                                                                                                                                                                                                                                                                                                183 NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57. 68
/note= "Conserved Cys-pairs identified N-terminal or
leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifreeze, perennial ryegrass; cold tolerance, transgenic; plant, antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for
                                                       5.
  Length 262;
                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conserved leucine-rich repeats"
Query Match 71.7%; Score 992.5; DB 8; Best Local Similarity 75.0%; Pred. No. 2.8e-79; Matches 198; Conservative 22; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perennial ryegrass antifreeze protein AFP5.
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 VSGSNNTVSGSNHIVSGSNKVVTD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 VSGSNNTVSGSNHVVSGSNKVVTD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifreeze proteins"
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The present sequence is that of AFP5, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall feecue) antifreeze proteins and the polynucleotides conciding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides were isolated from tissues taken tarts of the plants. The plants, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter. Sequence, into the genome of the organism, or introducing double-stranded CRNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopresservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a continual kindney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 NNSVSGSKNITVVSGNDNITVIGSNHVVSGTNHIVIDNNNNVSGNDNNVSGSFHIVSGGHNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 MAKCCMLLVFLGFILQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 SLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT
modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.8%; Score 980.5; DB 8; Length 2 Best Local Similarity 73.5%; Pred. No. 3e-78; Matches 194; Conservative 24; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifreeze; perennial ryegrass; cold tolerance;
antigout; litholytic; nephrotropic; cytostatic.
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/label= Signal_peptide
59. .70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSGSNNTVSGSNHVVSGSNKVVTD 253
                                                                              Claim 7; SEQ ID NO 23; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                            biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 254 AA;
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                      treating
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The present sequence is that of an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (whiter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded and are expected to the organism, or into the genome of the organism, or into the expansion of the organism, when the control or a gene promoter sequence, into the define of the organism, when the control or a sequence or the control or a sequence or the control or a sequence or the control or a sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                          /note= "7-amino acid sequence repeat region identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 MAKCCMLLVFLGFILQVAG---ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASC
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/note= "Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to protect a plant from damage due to frost or freezing.
                                                                 /note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                       Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID NO 25; 71pp; English.
                                                                                                                                  antifreeze proteins"
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                                                                                                                                                                                                                                                         09-SEP-2003; 2003WO-NZ000199
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Best Local Similarity 72.6*
Matches 193; Conservative
                                                                                  .255
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N-PSDB; ADM41469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 256 AA;
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patient e.g. tumour tissue, and to protect a plant from damage due
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             frost or freezing
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Peptide
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ADM41476
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                                                                                                                                                                                                                                                                                                                                                                             /note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of APP3, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41483-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                /note= "Conserved Cys pairs identified N-terminal of
leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                  transgenic; plant;
                                                                                                                                                                                                                                                                                                                                        69. .125
/note= "Conserved leucine-rich repeats"
161. .275
                                                                                                                                                                                                 Antifreeze, perennial ryegrass, cold tolerance, antigout, litholytic, nephrotropic, cytostatic.
             266
                        230 NTVSGSNNTVSGSNHVVSGSNKVVTD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fish SA;
                                                                                                                                                                                                                                                                           1. .23
/label= Signal_peptide
                                                                                                                                                                         Perennial ryegrass antifreeze protein.
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                                                                                                                                                                                                                                                              Location/Qualifiers
             NTVSGSNNTVSGSNHIVSGSNKVVTD
                                                                                                                                                                                                                                                                                                                                                                                           antifreeze proteins
                                                                                                ADM41477 standard; protein; 277 AA
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WRIGHTSON SEEDS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-2003; 2003WO-NZ000199.
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                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biocrystals (e.g. gout).
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             241
                                                                                                                         ADM41477;
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(WRIG-)
                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                      65 EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS 109
                                                                                                                                                                                                                                                                                      110 LVGEVPKSLOIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                     169 NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNN 228
                                                                                                                      64
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                                                                                                                                                                                                                                                                                                               5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                               Gaps

    53. 64
    /note= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"
69. 1124

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                                                                               19;
                                      Length 277;
                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                    Query Match 65.7%; Score 910.5; DB 8; Best Local Similarity 67.5%; Pred. No. 5.3e-72; Matches 187; Conservative 20; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 VSGSFHTVSGSHNTVSGSNNTVSGSNKVVT
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'label= Signal_peptide
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/note= ".
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Sequence 277 AA;
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N-PSDB; ADM41463,

Interest proteins and the polynucleotides encoding them ADM41458antifreeze proteins and the polynucleotides encoding them ADM41458ADM41483. The polynucleotides were isolated from tissues taken at
different times of year (winter and spring) and from different parts of
the plants. The polynucleotides can be used to modulate the cold
to clerance of an organism, especially plants, mammals, insects, fungi,
carchaea and bacteria. The method involves incorporating an antifreeze
polynucleotide, under the control of a gene promoter sequence, into the
copynucleotide into the cells of the organism, thereby inhibiting
to the polynucleotide into the cells of the organism, thereby inhibiting
expression of an antifreeze polypeptide. The antifreeze protein can be
cused for the cryopreservation of a cell or tissue, as a food additive of
a frozen food product, in a method for decreasing the time required to
calcabydrate a composition, to treat a disorder characterised by biocrysteals
cassociated with disorders such as gout and kidney stones, to preserve the
viability of a molecular biology reagent, to destroy unwanted tissue in a
copy front or freeing New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted present sequence is that of an antifreeze protein of Claim 7; SEQ ID NO 19; 71pp; English biocrystals (e.g. gout) rost or freezing Sequence 277 AA; 178 169 229 ADM41483; RESULT 8 셤 à g 원 ò ò 셤 à d

109 NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHLVTDNNNVVSGNDNN 228 57 5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW 65 EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS 110 LVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN transgenic; plant; Length 277; DB 8; VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265 VSGSSHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 274 65.6%; Score 908.5; DB 8; 67.9%; Pred. No. 8e-72; ive 19; Mismatches 51; Antifreeze, perennial ryegrass; cold tolerance; antigout; litholytic; nephrotropic; cytostatic. Perennial ryegrass antifreeze protein. ADM41483 standard; protein; 281 AA Query Match Best Local Similarity 67.9° Matches 188; Conservative (first entry) 03-JUN-2004

Location/Qualifiers 1. .19

Lolium perenne

Key Peptide

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The present sequence is that of an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tayegrass. The invention provides forage grass (perennial ryegrass and tall feature) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the polymucleotides can be used to modulate the cold of tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze of polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting cused for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to debydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the cryopreservations in a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the cryopreserve in the control of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                       'note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.
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                                    "Conserved lipoprotein membrane attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                        'note= "Conserved Cys-pairs identified N-terminal eucine-rich repeats of receptor-like kinases"
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8
                                                                                                                                 "Conserved leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%; Score 904.5; DB 66.5%; Pred. No. 1.8e-71 ive 20; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fish SA;
Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; SEQ ID NO 26; 71pp; English.
                                                                                                                                                                                            antifreeze proteins"
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Best Local Similarity 66.5*
Matches 187; Conservative
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                                                                                                                                     /note=
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expression of an antifreeze polypeptide. The antifreeze protein
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/note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of APP3, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a root cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting
SGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG 224
                     237
                                                                                                                                                                                                                                                                                                                   "Conserved lipoprotein membrane attachment site"
            SGNDNAVSGNDNTVICGNNNTVSGSNNTIASGSDNIVTGSNHIVCGTKHIITDNNNDVSG
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                                                                                                                                                                                                                transgenic; plant;
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leucine-rich repeats of receptor-like kinases"
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                                           265
                                                     NDNNVSGS FHTVSGEHNTVSGSNNTVSGSNH1 VSGSNKVVT
                                                                                                                                                                                                               Antifreeze; perennial ryegrass; cold tolerance; antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                          Perennial ryegrass antifreeze protein AFP3.
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/label= Signal_peptide
10. .22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fish SA;
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                                                                                                                                                                                                                                                                                                                                                                                                           antifreeze proteins"
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                                                                                                                       ADM41475 standard; protein; 281
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WRIGHTSON SEEDS LTD.
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used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                                                                                                                                                                                                                    Length 281;
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                                                                                                                                                                                                                                               65.1%; Score 901.5; DB 8;
66.2%; Pred. No. 3.4e-71;
ive 21; Mismatches 51;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note=
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                     frost or freezing
                                                                                                                                                                                                 Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004022700-A2
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Fish SA;

09-SEP-2002; 2002US-0409557P.

Perennial

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The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The encoding cDNA was isolated from a leaf blade cDNA expression library. The convertion provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADMA1458-CG ADMA1483. The polynucleotides were isolated from tissues taken at CG different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to omodulate the cold cold archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the cold archaea and bacteria. The method involves incorporating an antifreeze polynucleotide into the cils of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be conspected into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be conspected, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a cold fract or fract or fract a plant from damage due to
                                                                                                                                                                                         New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                          Claim 7; SEQ ID NO 22; 71pp; English.
                                   (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM41478 standard; protein; 280
                                                                                            Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                       biocrystals (e.g. gout).
                                                                                              Demmer J, Shenk MA,
                                                                                                                                 WPI; 2004-248453/23.
N-PSDB; ADM41466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frost or freezing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004
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ID ADM4
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AC ADM4
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DT 03-L
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                                                                                                                                                                                                                                               LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSV 163
                                                                                                                                                                                                                                                                         182 LSGRNNVVSGNDNTVISENNNTVSGSFNTVITGSDNVLTGSNHVVSGRSHIVTDNNNSVS 241
                                                                                                                                                                                                         62 NGASGRITTLWLPRRGLAGTITGASLAGLARLESLNLANNRLVGTIPSWIGELDHLLYLD 121
                                                                                                                                                                                                                                                                                                                              GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
                                                                                           69
                                                                                                                                 61
                                                                                10 MILVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
                                                                                                          Gaps
                                              27;
          DB 8; Length 285;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                            GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                      65.1%; Score 901.5; DB 8;
65.5%; Pred. No. 3.5e-71;
ive 17; Mismatches 54;
Query Match 65.1%
Best Local Similarity 65.5%
Matches 186; Conservative
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4;

Gaps

32;

Length 280;

63.8%; Score 884; DB 8; Length 280 65.5%; Pred. No. 1.2e-69; ive 14; Mismatches 52; Indels

Query Match
Best Local Similarity 65.5%
Matches 186; Conservative

Sequence 280 AA;

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The present sequence is that of AFP4, an antifreeze protein of perennial ryegrass. The encoding CDNA was isolated from a leaf and pseudostem CDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides contissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides were isolated from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded thereby inhibiting expression of an antifreeze polypeptide. The cattering antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a clisorder characterised by biocrystals associated with disorder such as contractive to destroy unwanted tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                  /note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                         12. .22
/note= "Conserved lipoprotein membrane attachment site"
52. .63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                          /note= "Conserved Cys-pairs identified N-terminal or leucine-rich repeats of receptor-like kinases"
                                  Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout, litholytic, nephrotropic, cytostatic.
                                                                                                                                                                                                                                                                             note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                 Transmembrane domain
 ryegrass antifreeze protein AFP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA;
                                                                                                                                          .. .22
'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; SEQ ID NO 21; 71pp; English.
                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2002; 2002US-0409557P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2003; 2003WO-NZ000199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WRIG-) WRIGHTSON SEEDS LTD
                                                                                                                                                                                                                                                                                        ....153
/note = Tr-
.65
                                                                                                                                                                                                                                                                68. .134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-248453/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to protect a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADM41465.
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                                                                                   Lolium perenne
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                                                                                                                         Key
Peptide
                                                                                                                                                                           Region
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different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107. .242
/note= "7-amino acid sequence repeat region identified in
antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 LTTAGRSLGKAPTNMPLHVKSSQGTLDEEHNTITGINNTVKSGSNNVVSGNDNTVISGNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEH--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Conserved lipoprotein membrane attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAKCWOLLLFLAFILPAASAA - SRHPDDLRALQDFAGNLRGGGVV - LRAALSGGSCCDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 LTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW

    .64
    /note= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"

    The polynucleotides were isolated from tissues taken at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 -------NTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                        53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASHSTISGNEDITVSGSNNFVSGNNNIVSGSNHVVYGNNKVVTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antifreeze, perennial ryegrass, cold tolerance, antigout, litholytic, nephrotropic, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                   Score 668; DB 8;
Pred. No. 1.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perennial ryegrass antifreeze protein AFP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .20
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.0%;
Matches 151; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 EGAGCDGASGRVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13. .23
/note= "
                                                                                                                                                                                                                                                                                                        rost or freezing
                                                                                                                                                                                                                                                                                                                                             Sequence 243 AA;
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ADM41471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                                              177 LSGRNNTVSGNDNTVISGNNNTVSGSFNTVVTGSDNVLTGSNHVVSGRNHIVTDNNNAVS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of an antifreeze protein of tall fescue. The encoding CDNA was isolated from a basal stem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-
                                                                                                                    121
                                                                                                                                                            LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDBEPNTISGTNNSV 163
                                                                                                                                                                                                 LSHNSLVGELP-----NLKGLTTTGHLLGMAFTSMPLDVKPNRRTLAVQPNTISGTNNSV 176
                                                                               --- GIIPSSIGELDHLRYLD 104
  69
                                         61
                                                                                                        GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS
MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
                      New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic; plant; antigout;
                                                                                                                                                                                                                                                                                                                                             GDDNNVSGSFHKVSGSHNTVSGSNNTVSGRNHVVSGSNKVVTGG 280
                                                                                                                                                                                                                                                                                                                      GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
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/label= Signal_peptide
                                                                             ETASGRUVALRLPKRGLG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fescue; cold tolerance; to nephrotropic; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM41472 standard; protein; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tall fescue antifreeze protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-2003; 2003WO-NZ000199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2002; 2002US-0409557P
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WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biocrystals (e.g. gout)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-248453/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifreeze;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Demmer J,
                                                                                                                    62
  20
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                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM41472;
                                                                                                                                                            105
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(WRIG-)
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DAMA1472

ADMA1472

ADMA14

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64; Gaps

RESULT

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Length 243;

64 57 124

-----SFOILLKG 78

183

243

transgenic; plant;

us-10-657-852a-15.rag

98WO-EP008553.

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Anti-freeze protein; grass; plant; frozen food product; frost tolerance;
                                                            Grass anti-freeze protein sequence
                                 29-SEP-1999 (first entry)
                                                                                                          frozen confectionery
                                                                                                                                    Lolium perenne.
                                                                                                                                                                                                                          23-DEC-1998;
                                                                                                                                                                 WO9937782-A2
      AAY22472;
      셤
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                                                                                                                                                                                                                                                                                                   The present sequence is that of APP1, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a pseudostem cDNA ryegrass and tall fescue) antifreeze proteins and the polymucleotides ryegrass and tall fescue) antifreeze proteins and the polymucleotides concoding them ADM41453-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, funst, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded and corresponding to the polymucleotide into the calls of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e; tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 LITDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGINNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAKCWQLLIFIAILIPPASAA--SCHPDDLYALRDFAGNIRG-GGVLLRAALPGASCCGW 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGVGCDGASGCV-----kSPQILLKG 78
                                                                                                                                                                                                      New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 SGSHSTVSGNHNTVSGRNNSVYGNNNIVSGSNHVVYGNNKVVTGG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.3%; Score 655; DB 8;
51.9%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                   Fish SA;
                                                                                                                                                                                                                                                                             Claim 7; SEQ ID NO 14; 71pp; English.
                                                                                      GENESIS RES & DEV CORP LTD
                                                                                                                                Demmer J, Shenk MA, Hall C,
                           09-SEP-2003; 2003WO-NZ000199.
                                                         09-SEP-2002; 2002US-0409557P
                                                                                                    (WRIG-) WRIGHTSON SEEDS LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 148; Conservative
                                                                                                                                                                                                                                                  biocrystals (e.g. gout).
                                                                                                                                                         WPI; 2004-248453/23.
N-PSDB; ADM41458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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18-MAR-2004
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This sequence is the plant anti-freeze protein of the invention. The anti-freeze protein is characterised in that at least 40% of its amino acids are from the group of serine, threonine and apparagine. The amino acids protein can be used in frozen food products, especially frozen confectionery. Anti-freeze proteins are especially infood products, on thich are heated, e.g. by pasteurisation, blanching or sterilisation prior to freezing. Plants transformed with a nucleic acid sequence encoding the anti-freeze protein have an increased frost tolerance. Prior at anti-freeze proteins have not been applied to commercially available food products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze proteins have tended to commercially available food products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze protein the pasteurisation step. This is overcome by the present anti-freeze protein. The anti-freeze protein confliction assay of 15 mu M or less. The anti-freeze protein ingredient means that mixes can be frozen under quiescent conditions, e.g. in a shop or minemally obtained via and hence with a texture different to products normally obtained via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 DEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTINHIVTDINININVSGNDININVSGSFHTVSGGHNTVSGSNNTVSGSNKVVTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                               New plant anti-freeze protein useful in frozen food products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.3%; Score 530; DB 2; Length 11
85.5%; Pred. No. 7.3e-39;
iive 10; Mismatches 7; Indels
                                                                                                                                                                          ö
                                                                                                                                                                      Worrall
                                                                                                                                                                      Twigg S,
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                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 36; 39pp; English
98GB-00001408
                                                                                                                                                                   Jarman CD, Sidebottom CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2002 (first entry)
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                                                                                                                                                                                                                                     WPI; 1999-458697/38.
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Best Local Similarity
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                                                                  (UNIL ) UNILEVER
(UNIL ) UNILEVER
                                                                                                                                                                                                                                                                    N-PSDB; AAX99717
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   22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim:
Matches 100;
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AAY22472 standard; protein; 118 AA

RESULT 14
AAY22472
ID AAY22
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Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEGSDVSGRVTKLVLPEKGLEGVISKSLGELTELRVLDLSRNQLKGEVPAEISKLEGLQV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 NDNTVV----SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG----- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 EIHPELCSSSGGIQVLDLSMNRLVGNLD----GLYNCSKSIQQLHIDSNRLTGQLPDYLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ILLVFF-----VGSSVSQPCHPNDLSALRELAGALKNKSVTE---SWLNGSRCCEWDGVF 56
                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                             comprising aligning and comparing nucleic acid or amino acid sequen
from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 SIRELEQLSLSGNY--LSGE---LSKNLSNLSGLKSLLISENRFSDVIPD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 30.7%; Pred. No. 1.6e-13;
Matches 89; Conservative 50; Mismatches 98; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 3015; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 KSLTTDSQSLGMGSI-NMLLHVSSRRTLDEEPNTISGTNNSVG-
                 Herbicidally active polypeptide SEQ ID NO 3015.
                                                       Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                                                   28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                           Tietjen K, Weidler M;
                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1036 AA;
                                                                                                                                                                                                                                                                                       (FARB ) BAYER AG.
                                                                                                                                 WO200210210-A2
                                                                                                                                                                     07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organisms
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Search completed: May 9, 2005, 20:20:40 Job time: 78 secs

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AUTHORS
TITLE
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COMMENT
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VERSION
KEYWORDS
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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9b_htc::
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Match Length
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EST 23-MAY-2002
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases I triticeae; Hordeum.
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23cto, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
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vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
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/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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Fax: 81-559-81-6855
Email: Lahini@enes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 372.8; DB 4;
llarity 73.5%; Pred. No. 4.2e-100;
Conservative 0; Mismatches 168;
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Center For Genetic Resource Information
National Institute of Genetics
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/tissue_type="leaves"
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CK197682
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BJ461731 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
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                                    /sub_species="vulgare"
/db_xere="rexon:112509"
/clone="baak32h16"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA lakashinriki vegetative stage leaves"
                                                                                                                                                                                                                      38.0%; Score 372.4; DB 4; 73.7%; Pred. No. 5.5e-100; iive 0; Mismatches 166;
/mol_type="mRNA"
/cultivar="Akashinriki"
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                                                                                                     ACTGACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGT---GAGCAGT 469
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
1 (bases 1 to 746)
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Barley EST sequencing project in NIG
Unpublished (2002)
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Location/Qualifiers
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 699)
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/clone lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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National Institute of Genetics
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/db_xref="taxon:112509"
/clone="baak46n01"
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Hordeum vulgare subsp. vulgare
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
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/clone_lib="K. Sato unpublished cDNA library, cv.
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                                                                                               1 (bases 1 to 666)
Sato,K., Saisho,D. and Takeda,K.
Barley BST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                              1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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|clone="baak46120"
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Location/Qualifiers
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
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/clone_lib="K. Sato unpublished cDNA library,
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/cultivar="Aksahinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Pred. No. 3e-98;
0; Mismatches 149;
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Barley EST sequencing project in NIG and
Unpublished (2002)
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/tissue_type="leaves"
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Hordeum vulgare subsp. vulgare
ISM Hordeum vulgare subsp. vulgare
ENKaryorda; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ENKaryorda; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

IS (bases 1 to 693)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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CTTGCCAACAACAGACTGGCTTGGCACCATCCCGTCATGGATTGGCGAGCTTGACCACCTT
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                                                                   /sub_species="vulgare"
|db_xref="texaon:112509"
|/clone="baak28d17"
|/tissue_type="leaves"
|dev_stage="vegetetive stage"
|dev_stage="vegetetive stage"
|Akashinriki vegetative stage leaves"
                                                                                                                                                                                                  ch 37.3%; Score 365.6; DB 4; Length 693; Il Similarity 75.3%; Pred. No. 5.9e-98; 503; Conservative 0; Mismatches 144; Indels 21
                            subsp. vulgare"
                            /organism="Hordeum vulgare
                                          /mol_type="mRNA"
/cultivar="Akashinriki"
location/Qualifiers
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BJ461908 K. Sato unpublished cDNA library, cv. Akashinriki BJ461908 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak21d01 3', mRNA sequence.

RESULT 7 BJ461908/c LOCUS DEFINITION

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                                                              Hordeum vilgare subsp. vilgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 696)
Sato, K., Saisho, D. and Takeda, K.
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Unpublished (2002)
Contact: Tadasu Shin-i
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/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                                                                                                                                                                                   Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 365.6; DB 4;
Pred. No. 5.9e-98;
0; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Akashinriki"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sub_species="vulgare"
|db_xref="taxon:112509"
|clone="baak21d01"
                                               Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="leaves"
GI:21140417
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Best Local Similarity 75.3%;
Matches 503; Conservative (
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BJ461908.1
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Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantes; Streptophyta; Engles; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (Dases 1 to 632)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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         CGCGTCGTGGCGTTGCGGCTCCCCAAGCGCGCCTTGGAGGGATCATCCCATCGTCGATT
                                                                                                 AATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGG
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Hordeum vulgare subsp. vulgare
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Location/Qualifiers
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BJ453251
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/wol type="mrNa"
/wol type="mrNa"
/cultiva="Chinese Spring"
/db xref="taxon:4565"
/clone="WHE0365_G07 N13"
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/dev_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/dev_stage="Five-day old seedling"
/dot="vector: Lambda Uni-ZAP XR. excised phagemid;
/note="vector: Lambda Uni-ZAP XR. excised phagemid;
/note="vector: Lambda Uni-ZAP XR. excised phagemid;
/site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, Germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Five-day old seedlings were transferred to 5 c
cold room and kept for 48 hr. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, the CDNA clones were in vivo excised to give pBluescript
phagemids in the TV Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                  BE490074 588 bp mRNA linear EST 31-JUL-2000 WHE0365_G07_N13ZS Wheat cold-stressed seedling cDNA library riticism aestivum cDNA clone WHE0365_G07_N13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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The structure and function of the expressed portion of the wheat genomes - Cold stressed seedling cDNA library
Unpublished (2000)
    856
                                                                                       857 TIGCTICCAICTICCCAAGIICAGIGAGCTTACAAICAAIAGAIGAGAGAAAICACGII 916
                                                87
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                          86 GCTCACCTTGTTGTCCGAGTTCGGTGTAGCTCACAATCACTTGGTGGGGCCAATCGTGT
AGCAACAAAGTCGTAACAGATGGTTAATAT--------TCTGTAGGTGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 5105559818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
37.0%; Score 362.4; DB 2; Length
Best Local Similarity 79.5%; Pred. No. 5.2e-97;
Matches 455; Conservative 0; Mismatches 111; Indels
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Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
1 (bases 1 to 671)
Sato, K., Saisho, D. and Takeda, K.
                                                                                                                                                  300
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                                                                                                                                                                                                                                                                                                             CCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGT---GAGCAGTAGAAGAAC 477
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BJ454271 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
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/dev_stage="begetative stage"
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Akashimriki vegetative stage leaves"
                                                                                              632;
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Barley EST sequencing project in NIG and Okayama Univ
                                                                                              Length
                                                                                                                       Indels
                                                                                            Score 362.2; DB 4;
Pred. No. 6e-97;
0; Mismatches 133;
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BJ454271.1 GI:21132845
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ilarity 77.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 AATTCATTGGTTGGCGAGGTACCCAAGAGTTT---GATACGGCTCAAGGGCTTCGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 AGCAACAATGTTGTTTCCGGGAATGACAACGCGCTCGTATCTGGGAATAACAACCATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 GCTGGGAGCAACACACTATCGTAACCGGGAACGACAATACCGTAACTGGTAGCAACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAATGTGTGTGTGGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGC
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/db xref="taxon:112509"

/clone="baak46n01"

/tissue-leaves"

/dw stage="vegetative stage"

/clone_lib="K. Sato unpublished cDNA library,

Akashinriki vegetative stage leaves"
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Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Bmail: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 359.4; DB 4;
Pred. No. 4.2e-96;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Akashinriki"
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EST 23-MAY-2002
                                           Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
1 (bases 1 to 609)
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            ATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATAT
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/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
TILL Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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/mol_type="mRNA"
/cultivar="Akashinriki"
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0; Mismatches 113;
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/db_xref="taxon:112509"
/clone="baak28d17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ462238 K. Sato unpublished cDNA library, cv. Akashinriki bBJ462238 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak24916 3', mRNA sequence.
BJ462238 GI:21140745
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Hordeum vulgare subsp. vulgare
Eukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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Akashinriki vegetative stage leaves"
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                                                                                                                                                                                                                                                                                                                                                                                         Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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|mol_type="mRNA"
|cultivar="Akashinriki"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
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Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Boales; Poaceae;
Booideae; Triticeae; Triticum.
1 (baess I to 692)
Anderson, O.D., Cheo, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Haia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
Unpublished, (2000)
                                                                                   445
                                                                                                                                                                                                                                                           325
                                                                                                                                                     444 AACAACACTGTCAGATCTGGGAGCACCAATGTTGTTTCTGGGAACGACACACTGTCATA 385
                                                                                                                                                                                                                                                                                                   632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT 691
                                                                                                                            512 AACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCGTA 571
                                                                                                                                                                                                                572 TCTGGGAATAACAACCATGTGTGTGTGAGCAACAACACTGTTGTAACTGGAAGTGACAAT 631
                                                                                                                                                                                                                                                                                                                                              324 ACCGTAACTGGTAGCAACCATGTCGTATCTGGGGACAAAACATATCGTAACTGACAACAAC 265
                                                                                                                                                                                                                                                                                                                                                                                         692 AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG 751
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564 CGGCTCAAGGGCTTCGCCATCGCTGGTCGTTCATCAGGTATGATTTTTACTAACATGCCA 505
                                                                 504 TIGIATATGIGGAGCCTAACAGAAGAATGCTCGACGAACAACCAAATACAATATCTGGGAGC
                                                                                                                                                                                                                                             WHE0840 DOI H022S Wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0840 DOI H02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               752 CACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGG
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/dev stage="Five-week old seedling"
/lab_host="E. coll SOLR"
/clone lib="Wheat vernallzed crown cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stradgene SK primer.
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800 Buchannan Street, Albany, CA 94710, USA
TTE1: 5105595773
Fax: 5105595818
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Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaee; Hordeum.
1 (Dasses 1 to 689)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
                                                                                            386 ACCGTAACTGGTAGCAACCATGTCGTATCTGGGGACAAACATATCGTAACTGACAAC 445
                                                                                                                                              AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGAG 751
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BJ488121 K. Sato unpublished cDNA library, cv. Akashinriki
Vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baakl30m05 3', mRNA sequence.
                                                          ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT
                                                                                                                                                                       TCCGGGAACAACAACAATGTGGCTGGGAGCAACAACACTATCGTAACCGGGAACGACAAT
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/db_xref="taxon:112509"
/clone="baak30m05"
/tissue_type="leaves"
/clone_lib="K. Sato unpublished cDNA library,
Akashimriki vegetative stage leaves"
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|mol_type="mRNA"
|cultivar="Akashinriki"
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Pred. No. 2e-95;
0; Mismatches 113; Indels
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National Institute of Genetics
1111 Yara, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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ΚIA

Ontario,

Ottawa,

/mol_type="mRNA"
cuttivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="sc02 07e09"
/tissue_type="leaf, crown"
/dev stage="seedling three-leaf stage"
/clone_lib="sc02_AAFC_ECORC_cold_stressed_winter_rye_seedlings"

'organism="Secale cereale"

Bmail: singhja@agr.gc.ca.
Location/Qualifiers

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Sampled three-leaf seedlings treated for cone week at 2oC, 12 hrs light/day. Library made with Stratagene UNIZAP XK Kit/(not packaged). cDNA is directly ligated into SK+/XhoI-EcoRI, then electroporated into TOPIO cells (Invitrogen)."

612 355

Gaps

9

Length Indels

35.5%; Score 348.2; DB 2; 75.5%; Pred. No. 9.8e-93; ative 0; Mismatches 143;

Similarity

ĠAĂTCCTTGGCĂĠGCCTCĠCGCĠGCTGĠAĠGCTCAACĊTTGCCĂĂCAACAĠACŤGGTC

GGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGT 415

552

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532

AGAACGCTCGATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGG

GACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGAGCAGTA---GA

592

255

772 135 832

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551 AATTCATTGATTGGCGAGGTGCCCAAGAGTTT---GATACGGCTCAAGGGCATCGTCATC 495
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     Contact: Singh,J.A.
Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm,
OCG., Canada
TTel: (613) 759-1662
Fax: (613) 759-1701
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Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
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Secale cereale
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Secale (rye)
Spermatophyta; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Secale.

1 (bases 1 to 703)
Singh,Jd.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
                                                                                                                                                                                      SC02 07e09_A SC02_AAFC_ECORC_cold_stressed_winter_rye_seedlings
Secale cereale cDNA clone Sc02_07e09, mRNA sequence.
BE705098.1 GI:10093363
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

DEFINITION

Search completed: May 11, 2005, 01:33:58 Job time : 3917 secs This Page Blank Tusploj

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291 TTGGAGGGATCATCCC 306
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-232-463-14

US-10-101-464A-211

US-09-336-447A-6

US-09-952-267B-6

US-09-952-267B-6

US-09-434-288-12

US-10-101-464A-865

US-10-101-464A-865

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US-10-101-464A-819

US-10-101-464A-817

US-09-28-986-39

US-10-101-464A-817

US-09-28-986-39

US-10-101-464A-817

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US-09-072-596-171
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Sequence 19, Appl Sequence 7, Appli Sequence 12912, A Sequence 655, App Sequence 841, Appl Sequence 10, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appli Sequence 1219, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli	cells n of Plant Cell Signaling	Length 3453; Indels 0; Gaps 0;	AGGTGGCAGGACGT 110 	regergabacerabges 170 	CCTCATGCTGCAGCTGGGAAG 230	3GCTCCCCAAGCGCGGCC 290 A ACCTCTCCGGCGCCAACC 242	
US-09-657-440-19 US-09-249-180-7 US-09-270-767-12912 US-09-902-540-565 US-10-101-464A-841 US-09-105-537-30 US-09-105-537-30 US-09-105-537-5 US-09-105-537-5 US-09-320-878-19 US-09-320-878-19 US-09-330-878-19 US-09-336-447A-10 US-09-336-447A-10 US-08-336-4778-10 US-08-557-440-19 US-08-36-4778-10 US-08-36-4778-10 US-08-567-375-11	ALIGNMENTS 11464A 12 s Isolated from Plant 10/101,464A 4,302 8,986 2,866 2,866 Stool 00724	; Score 44.8; DB 4; ; Pred. No. 0.002; 0; Mismatches 132;	caagigitigcaigciggiciiciiciiciicaggiicaiciicgcaggigggaggaacgi 	cgregregrecaccaccaccacccreacgcgrraagggccregcreagaaccraagg 	gcaaagaagcgrccaccrccagcacagargccaggcacrcaracragaagagaaag 	grgraggaraccaaaacagcaagccacgrcgragcgrraccagcrcccaagcgcagcc 	900
8 38506 4 657 3 3 657 3 3 657 3 3 8506 4 8 21463 4 4 8 21463 4 4 2561 4 4 7 3 8506 4 3 8506 4 3 8538 4 4 6256 2 7 6256 2	ADJICATION US/10101464A Application US/10101464A BAPDICATION: rabala, Timothy rieuwenhuizen, Nicolaas liggins, Colleen M. NYION: Compositions Isol NYION: and Their Use in NYION: and Their Use in E: 11000.102022 CATION NUMBER: 09/104,302 DATE: 2000-11-01 TION NUMBER: 09/128,986 DATE: 1999-01-12 DATE: 2000-01-11 DATE: 2000-01-11 DATE: 2000-01-11 DATE: 2000-01-11 DATE: 2000-01-11	4.6% larity 48.4% Conservative	STIGCAIGCIG TCTIICCIIC	cgresrcgreccaccac 	BAGCCGTCCGC ACTCCTCCTC	gatgcgaaaca ggtgcgaccgc	
7.7.7.0 9.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A PACE PRO I COMPANDE PRI I COMPANDE PRO I COMPANDI	Simi 4;	51 CAAAGT(3 CAATGT	111 CGTGGT(171 GCAAAG 	231 GTGTGG 183 GCGTCG	740048 100
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-10-101-464, Sequence 86, RETEAL INF. APPLICANT: APPLICANT: APPLICANT: TITLE OF II FILE OF II FILE REPER APPLICANTE: FILE OF II FILE REPER APPLICANTE: FILE OF II FIL	Query Match Best Local 8 Matches 12	y da	රු අ	S G	oy B	ä

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## APPLICANT: Strabala, Timothy
## APPLICANT: Strabala, Timothy
## APPLICANT: Strabala, Timothy
## APPLICANT: Nieuwenhuizen, Nicolaas
## APPLICANT: Nieuwenhuizen, Nicolaas
## APPLICANT: Nieuwenhuizen, Nicolaas
## APPLICANT: Nieuwenhuizen Nicolaas
## APPLICANT: Nieuwenhuizen Nicolaas
## TITLE OF INVENTION: Compositions Isolated from Plant Cells
## TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
## TITLE OF INVENTION: 2000-12-2
## PRIOR PELING DATE: 2000-11-01
## PRIOR PELING DATE: 1999-01-12
## PRIOR FILING DATE: 1999-01-01
## PRIOR FILING DATE: 1999-11-01
## PRIOR FILING DATE: 2000-01-11
## NUMBER OF SEQ ID NOS: 989
## SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, Nicolaas
APPLICANT: Mieuwenhuizen, M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PLING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
                                     694 TGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 TCGATGGAAGCATCCCTTTTTGGATGGGGAAGATGGAGAACTTGTTTTATTTGGATCTGT 173
                                                                                                 754 CAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 TTGGAGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                   814 CAACAAAGTCGTAACAGATGGTTAATATTCTGTAGGTGCAGGATTGCT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 408;
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35; Indels
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Pred. No. 0.0087;
0; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                       Sequence 212, Application US/10101464A
Patent No. 6768041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 221, Application US/10101464A Patent No. 6768041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.9%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Strabala,
                                                                                                                                                                                                                                                                                                                                                          US-10-101-464A-212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 CAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCGTATC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 TGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATAC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 TGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAATAA 693
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4.6%; Score 44.8; DB 1; Length 7218;
Best Local Similarity 4.7%; Pred. No. 0.0033;
Matches 19; Conservative 216; Mismatches 173; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INPORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
                  243 TCGGCGGCCCTTCCC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14
                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                       US-08-232-463-14/c
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961 CCAACAACGCCGTCGCTCTAGGTAAAATAACACCATCGATGGCGATAACTCAGTAGCCA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 crcaraaccaacacacadergaagerrcarrrecaedagergradagaadcaaaccaare 960
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/249,180
CURRENT FILING DATE: 1999-02-12
EARLIER APPLICATION NUMBER: 60/076/014
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Created in Patentin Ver. 2.0, Edited in WordPerfect 6.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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4.1%; Score 40.4; DB 4; Length 3381;
Best Local Similarity 46.5%; Pred. No. 0.054;
Matches 131; Conservative 0; Mismatches 151; Indels 0.
          1021 TCGGCTCTAATAATACCATTGACAGTGGCAAACAAAATGTCT 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 rcescrcrahrahakcahrsacasrescaaacaaarshcr 1062
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                                                                                                                                                                           Sequence 6, Application US/09952267B
Patent No. 6753417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 3381
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                               US-09-952-267B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 CAGGCGAGAATCAACGGTTGCAGGGGCAGGAATAACCAAGCCACAGGCAACAACACTCAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 CGGTTGCAGGCGGCTCTTATAACCAAGCCACAAGACAACTCAACGGTTGCAGGTGGTT 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 CCTCGAGGTGCTCTGGCTCAGCGAGTGCGGCCTGACCGGGAAGATCCCGGAGTCGCTCGG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 GAGGCTCAAGAGGCTCACCGATTTGGACCTCGCCTTCAACTACTTGGAGGGCCCCATACC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 CGGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAA 623
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| Patent No. 6310190
| GENERAL INFORMATION:
| APPLICANT: HANSEN, ERIC J.
| APPLICANT: AEBI, CHRISTOPH
| APPLICANT: MACTVER, ISOBEL
| APPLICANT: FISKE, MICHAEL J.
| APPLICANT: FISKE, MICHAEL J.
| APPLICANT: FISKE, MICHAEL J.
| APPLICANT: PREDENBURG, ROSS A.
| TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
| FILE REFERENCE: AMCY:024
| CURRENT APPLICATION NUMBER: US/09/336,447A
| UNMBER OF SEQ ID NOS: 98
| SOFTWARE PATENTIAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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4.1%; Score 40.4; DB 3; Length 3381;
Best Local Similarity 46.5%; Pred. No. 0.054;
Matches 131; Conservative 0; Mismatches 151; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.1%; Score 40.4; DB 4; Length 396;
Best Local Similarity 58.2%; Pred. No. 0.013;
Matches 71; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 CAGGGGAGCACATACCGTATCCGGGAGCAACAATACTGTAT 785
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 221
LENGTH: 396
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                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-101-464A-221
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US-09-336-447A-6
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                                                                                                                                                                                                                                                                                                                                                                                             85 CATCTTGCAGGTGGCAGGAACGTCGTGGTCGTGCCACCACGACGACCTCCACGCGTT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 GAGGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCGTCCGCCTCCGCGCCGCATGGTC
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56.2%; Pred. No. 0.16;
cive 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                        Score 38.8; DB 3;
Pred. No. 0.11;
0; Mismatches 97;
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PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 840
LENGTH: 2900
                      FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
        CONSTRUCTS THEREFOR
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Patent No. 6768041
                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-12
                                                                                                                                                                                                                                                                                                          4.0%;
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Best Local Similarity 50.0°
Matches 97; Conservative
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Matches 73; Conservative
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        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AGTAGCCGGCGCCTCCGCGGCTACAACACCGGCGCTCCGCTCCGACGCTACGAGGGGGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 GGGATGCGAAACAGCAAAGCGGCCGCGTGGCGTTGCGGCTCCCCCAAGCGGGGCCTTGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 CGAGTCGGAAGACGATAGCGTCCGCGAGTACGATGGGCGGCGGCGGCGGGGGGGACTACGC 308
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| Patent No. 6303767
| GENERAL INFORMATION:
| APPLICANT: Betlach C., Melanie
| APPLICANT: McDaniel, Robert
| TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
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Pred. No. 0.083;
0; Mismatches 77; Indels 0
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AUTHORS: Blthon, Thomas E.
TITLE: Heat-Stress Response of Maize Mitochondria
JOURNAL: Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(1028)
OTHER INFORMATION: Zea Mays L., Line B73
                                                                                                                                                                                             ION: (424) ..(693)
INFORMATION: Heat Shock Domain
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Matches 85; Conservative
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LOCATION: (79)..(213)
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"UBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Poly A site
LOCATION: (1028)..(1028)
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LOCATION: (736)..(1028)
                                                                                                                                                                       NAME/KEY: misc_feature
                                          CDS
(79)...(735)
                                                                                                                            (1)..(1028)
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Zea mays
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PAGES: 1097-1110
DATE: 1998-03-00
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Micolaas
APPLICANT: Nieuwenhuizen, Micolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11000-11020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
FILE OF INVENTION NUMBER: US/10/101,464A
FROR APPLICATION NUMBER: 09/704,302
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use 1090/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SEQ ID NO 39
LENGTH: 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 CGTGGTCCCGCGGCGGCCGACCCCTGCGGCGCGCGCGCGTCGTTCGAGGGGGTGGCGTGCG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 AAACAGCAAGCGGCCGCGTCGTGGCGTTGCGGCTCCCCAAGCGCGGCTTGGAGGGATCA 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 TCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCAT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 TCCGCCTCCGCGCCGCATGCTCCGGCGCCTCATGCTGCTGCAGGTGTGGGAAGGTGTGGGAATGCG
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CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6359198
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CRGANISM: Eucalyptus grandis
US-10-101-464A-865
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Nicolaas
APPLICANT: Higgins, Collean M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPRENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/J0/101,464A
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR PLING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-01-11
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Patent No. 6768041

GENERAL INPORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nicolaas
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1783 TCAGGACATGGATTTCTCCTCCAACAAATTGTCAGACTTGGACTTCAAAGCTTTGATATT 1842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 268, Application US/10101464A patent No. 6768041
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ORGANISM: Eucalyptus grandis
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                                                                                                                          394 ACGCCTCAAG 403
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US-10-101-464A-268
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US-10-101-464A-865
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PRIOR FILING DATE: 2000-01-11
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Best Local Similarity 51.5
Matches 88; Conservative
                                                                                                        TYPE: DNA
ORGANISM: Pinus radiata
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US-09-621-976-15639
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                                                                                                                                                 US-10-101-464A-421
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                                                                                     LENGTH: 498
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Best Local S
Matches 54
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                                                                                                                                                                                                                   APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Biggins, Colleen M.
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION TOOG-102022
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
PRIOR PLILOR DATE: 1999-01-12
PRIOR PLILNG DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR APPLICATION NUMBER: E0/162,866
PRIOR PLING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 989
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APPLICANT: Strabala, Timothy
APPLICANT: Miscuenthuizen, Nicolaas
APPLICANT: Miscuenthuizen, Nicolaas
APPLICANT: Miscuenthuizen, Nicolaen
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2 us. 18010/101,464A
CURRENT APPLICATION NUMBER: 09/704,302
FRIOR APPLICATION NUMBER: 09/704,302
FRIOR APPLICATION NUMBER: 09/28,986
FRIOR FILING DATE: 1999-01-12
FRIOR FILING DATE: 1999-11-01
FRIOR FILING DATE: 1999-11-01
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297 CCCTGAGTGCTGGTTGAATGGTACGCTCTCCCCGTATATTGGGAACCTCCTCTTTTGCG 356
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                                                                               357 GCATTTAGATCTTTCTTGGAATGCTTTGAGTGGGAGAATTCCAGCAGAGTT 407
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                                        337 CTATTTGGATCTCTCGGGTAATTCATTGGTTGGGGAGGTACCAAAAGTTT
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Thes 83; Indels
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51.5%; Pred. No. 0.0
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; Sequence 421, Application US/10101464A
; Patent No. 6768041
                                                                                                                                                                                 Sequence 39, Application US/10101464A
Patent No. 6768041
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Matches 88; Conservative
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ORGANISM: Pinus radiata
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                                                                                                                                                                                                                                  Score 38.2; DB 4; Length 498;
Pred. No. 0.081;
0; Mismatches 83; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15539
LENGTH: 505
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
                                                                                                                                                                                                                                  3.9%;
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604 CAACACTGTTGTAACTGGA 622

604 CAACACTGTTGTAACTGGA 622 ::: || :| || :| || 425 YMWTTCTCWTWTWYGTTRA 443

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Search completed: May 11, 2005, 02:55:00 Job time : 221 secs

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Acn45174 Human gen Aba70168 Plasmodiu Abl17081 Drosophil Abd17272 Oligonucl Abd17273 Oligonucl Abd17273 Oligonucl Aba79411 Eucalyptu Aba79410 Eucalyptu Aba79420 Eucalyptu Aba79420 Eucalyptu Aba79420 Eucalyptu Aba79420 Eucalyptu Aba79432 Human exc Aba81183 DNA encod Adm80069 Spiramyci Adm80069 Spiramyci Adm80034 Spiramyci Adm80034 Spiramyci

Ada71938 Rice gene Abl18481 Drosophil Adm03281 Human cDN Abl18480 Drosophil

Abz23668 H. pylori Abl17081 Drosophil Abl17080 Drosophil Aaa50251 Maize hea

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

<u>e</u>

Sequence:

us-10-657-852a-3.rng

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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                          Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout, litholytic, nephrotropic, cytostatic, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Antifreeze protein AFP2"
                                                                                                                                                                                                                                                                                                                                                                         Perennial ryegrass antifreeze protein AFP2 cDNA.
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ABL17081
ABL17080
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ADM90069
ADM97585
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                        The present sequence is that of cDNA encoding AFP2, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polyuncleotides ryegrass and tall fescue) antifreeze proteins and the polyuncleotides or choose taken at different times of year (winter and spring) and from different parts of the plants. The polyuncleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polyuncleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polyuncleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The crissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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846 894 906 954 996

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667 CGTATCAGGGACAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAA 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feacue; cold tolerance;
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(WRIG-) WRIGHTSON SEEDS LTD
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                            The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression labrary. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of agene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kindey stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 904.4; DB 12; Length
Pred. No. 5.2e-273;
0; Mismatches 31; Indels
SEQ ID NO 4; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.3%;
Best Local Similarity 96.2%;
Matches 949; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 996 BP; 268 A; 235
                                                                                                                                                                                                                                                                                                                                                                                                                      frost or freezing.
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present sequence is that of cDNA encoding an antifreeze protein (fescue. The cDNA was isolated from a leaf blade cDNA expression
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Sequence 1006 BP; 248 A; 261 C; 260 G; 237 T; 0 U; 0 Other;

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	-	28.	SGTCTTC	GACGA	H H	CTCCGC	CTTCG	GCAAG	GCCAG	VICGIC	TCGTG	GGGGAC	GGCGAC	CTCGG	-E	GAAGA	GAGCAC	GTTTC	GTTGC	AACAC	AACAC	SACAAAC	ACAAAC	GGAAGO
	Length	grapi	TCTTGTTCAATCCATGCCTGAATACATGGCAAAGTGTTGCATGCTGGTCTTCTTGGG	GTTCATCTTGCAGGTGGCAGGAGCAACGTCGTGGTCGTGCCACCACCACGACGACGTCCA	GTTCCTCTTGTCGGCGGCTGGCACGGCGACGCCACGCCA	CGCGTTGAGGGGCCTCGCTGAGAACCTAAGCGCAAAAGGAGCCGTCCGCCTCCGCGCGC	TGCGCTGCGGGGCTTCGCTGAGAACCTGGGCGCGCGCGCG	ATGGTCCGGCGCCTCATGCTGCAGCTGGGAAGGTGTGGGAATGCGAAACAGCGGCCG	GIGGICAGGCGCCTCATGCTGCGATTGGGAAGGCGTTGGCTGCGACGGTGCCAGCGGCCC	CGICGIGGCGTIGCGGCTCCCCAAGCGCGCCTITGGAGGATCAICCCATCGTCGTTGG	TGTCACGGCTTTGTGGCTCCCCAGGGGCGCCTCACGGGGCCAATCCCTTGGTGGATTG	TGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCATTGGTTGG	TCAGCTTCACCACCTACGCTACTTGGATCTTTCAGGTAATGCATTGGTTGG	AAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGG	CAAGAATCTGCAGGTACAGGCTCAAAGGCCTCACCGCTGCCGGTC	TICCATIAACAIGCIAIIGCAIGIGAGCAGIAGAAGAACGCICGAIGAAGAACCAAA	TTTCACCAACATGCCATTGCATGTGATGCGTAACAGAAGATCACTCGACGAGCAGCACAA	TACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAA		TGACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGCAACACACTGTTGT		AACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATAT	A GOGG GOOD AND THE CONTRACT GOOD AND THE CO	Grerci
	٠.	:: ::	GCATO	CGTGC	CATG	GAGCC	- - - - - - - - - - - - - - - - - - -	GATG	SGCTGC	GGATC	3GCC2	ATTC	ATGC	ACAGO	- - - - - - - - - - - - - - - - - - -	GAACG	GATC	GCAAC	GCAAA	CTGG	CTGG	TCGTA	TCGT	ATAAT
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	•	5	SCCTGA	GCAGG	GCTGG	GCTGA	CCTGA	TGCTG	TGCTG	SCTCC	CTCC	CGCTA	CGCTA	CGGCT	CAGCT	VITGCA	TTGCA	PACAA	AACAA	VICTGG	VICTGG.	ACTGT	ACCGT	PAATGT
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	larity 76.) IBEL	STTCAA	ATCTTG	TCTTG	rtgagg	TGCGG	CCGGC	CAGGC	STGGCG	ACGGCT.	TTGAT	TTCAC	AGTTTG	ATCTG	ATTAAC	CCAAC	TATCA	TATCT	ACACG	ACACC	SGAAGT	3GGAGT(ACTGAT
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679 CGTTACAGACAACAATAACGTATCCGGGAACGATAATAATGTATCCGGGAGCTTTCA 738
                            795
                                                     798
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                                                                                                                                                                                                                   919 TTGGTGCGTTCAATCGCGTTATGTAACTTCATGGATATACCATACTTTTCCTACTATATA 978
                                                                                                         799 ccargriciarcregaagcaacaacaaercereacaececriaarearcrereacecare
                                                                                                                                     --- CCCAAGTTCAGTGTAGCTTACAATCAA
                                                                                                                                                               859 ATTGTTTCCACCTTAACTGAGCTCACGTTCTTGTCCAAGTTCACTGTACCTCACAGTCAG
                                                                                                                                                                                        TAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATACTTTTC---CTTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).
                          TACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAA
                                             TACCGTATCCGGGGGGCACAATACCGTCTCTGGGAGCAACAATACCGTATCTGGGAGCAAA
                                                                                CCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTGTAGGTGCAGG
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                                                                                                                                                                                                                                            TAAAGCTTCCCTTTACATAAAAAAA 980
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P-PSDB; ADM41480.
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The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifrese proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from
                                                                                                                                                                                                                                                                                                                                       911 TCACAGTCAGTTGGTGCGTTCAATCGCGTTATGTAACTTCATGGATATACCATACTTTC
                                                                                                                            791 CTGGGAGCAACCACGTTGTATCTGGAAGCAAAGTCGTGACAGACGCTTAATGATCTG
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ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1008 BP; 256 A; 265 C; 251 G; 236 T; 0 U; 0 Other;
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0; Mismatches 194; Indels
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different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATCAAGGTTTCTTGTTCAATCCATGCCTGAATACATGCCAAAGTGTTGCATGCTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%; Score 492.8; DB 12; Length ilarity 73.6%; Pred. No. 1.2e-143; Conservative 0; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 492.8; DB 12
Pred. No. 1.2e-143;
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                                                                                                                     844 GATCTGTCAGCGCATGATTGTTTCCACCTTAACTGAGCTCACGTTCTTGTCCAAGTTCAC
        784 CCGTATCTGGGAGCAACCACGTTGTATCTGGAAGCAACAAGTCGTGACAGACGCTTAAT
                                                                                                                                                                               TGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fescue; cold tolerance; transgenic; plant; antigout; nephrotropic; cytostatic; gene; ss.
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genome of the organism, or introducing double-stranded RNA corresponding
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                                                                                                                                                                                                                                   Length 1230;
                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                               Sequence 1230 BP; 327 A; 279 C; 298 G; 326 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    0; Mismatches 198; Indels
                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                                          33 CCATGCCTGAATACATGCCAAAGTGTTGCATGCTGCTGGT
                                                                                                                                                                                                                               Score 451.2; DB 12
Pred. No. 1.5e-130;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 72.0%;
Matches 708; Conservative
                                                                                                                                                              or freezing.
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--TGCAGGATTGCTTCC
                                 893 TGACAGGAGATGAATGATTTGTCAGGGGATCGTTTCCATCTTCCCTAAAGGAGCACTCAC
                                                                    865 ATCTTCCCAAGTTCAGTGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                        transgenic; plant;
gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Antifreeze, perennial ryegrass, cold tolerance, antigout, litholytic, nephrotropic, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Antifreeze protein"
                                                                                                                                                                                                                                                                                                                                                          Perennial ryegrass antifreeze protein cDNA
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 825 TAACAGATGGTTAATATTCTGTAGG-
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/product=
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/*tag= a
128. .889
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decreasing the time required to sorder characterised by biocrystals
                               preserve the
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          dehydrate a composition, to treat a disorder characterised by biocryst associated with disorders such as gout and kidney stones, to preserve viability of a molecular blology reagent, to destroy unwanted tissue i patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                                                                                                                           CATGCTGCGCCTGGGAAGGTGTGGCGCTACGTACAAGCGGCCGCGTCACGGCGTTGC
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                                                                                                                                                                             Gaps
                                                                                                                                                                          177;
                                                                                                                                              DB 12; Length 1212;
                                                                                                              Sequence 1212 BP; 326 A; 274 C; 287 G; 325 T; 0 U; 0 Other;
                                                                                                                                                                            Indels
                                                                                                                               45.3%; Score 443.6; DB 12; 71.2%; Pred. No. 3.7e-128; Nismatches 209;
in a method for
                                                                                                                                                                             Conservative
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Matches 706; Conserv
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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them the polynucleotides were isolated from tissues taken and it miss of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold to rolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gane promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding capression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of the car frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the
                                936 CTTGTCCAAGTTCAGTGCAGCTCACAATCACTTGGTAGGGGCAATCGAGTTATGTAACTT
866 TCTTCCCAAGTTCAGTGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antifreeze proteins and encoding polymucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                 fescue; cold tolerance; transgenic; plant; antigout;
nephrotropic; cytostatic; gene; ss.
                                                                                    "Antifreeze protein"
                                                                 CA-GGATATGGCATACTTTTCCTTTAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 9; 71pp; English.
                                                                                                                                                                                                                                                                                antifreeze protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                  BP.
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                                                                                                                                                                                  CDNA; 1246
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(WRIG-) WRIGHTSON SEEDS LTD.
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104. .907
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P-PSDB; ADM41479.
                                                                                                                                                                                  ADM41466 standard;
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                                                                                                                                                                                                                                                                                Tall fescue
                                                                                                                                                                                                                                                                                                                                                                 Schedonorus
                                                                                                                                                                                                                                                                                                                 Antifreeze;
                                                                                                                                                                                                                                                                                                                                  litholytic;
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                                                                                                                                                                                                                                                                                                                                                                                                    ATGGCGCGAGCGGCCGCATCACCACGTTGTGGCTCCCTAGGCGTGGCCTTGCGGGGACCA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACCACACAGGTCATTTACTAGGTATGGCTTTCACTAACATGCCATTGGATGTGAAGC 536
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viability of a molecular biology reagent, to destroy unwanted tissue in patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                         TCCTCCTCCGCACGCGTGGTCCGGCACCTCGTGCTGCTGCGAAGGTGTTGGATGCA
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                                                                                                           Length 1246;
                                                                                                                                              103;
                                                                       Sequence 1246 BP; 313 A; 294 C; 307 G; 332 T; 0 U; 0 Other;
                                                                                                       Score 421.8; DB 12; Length
Pred. No. 2.7e-121;
0; Mismatches 192; Indels
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                                                                                                           43.0%;
                                                                                                                        Best_Local Similarity 70.1%;
Matches 690; Conservative
                                     frost or freezing.
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                                                                                                       Query Match
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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                      transgenic; plant;
                                                                                                                      Antifreeze; perennial ryegrass; cold tolerance; transgeni
antigout; litholytic; nephrotropic; cytostatic; gene; ss.
                                                                                                                                                                                      "Antifreeze protein"
                                                                                                     Perennial ryegrass antifreeze protein cDNA.
               1041
                                                                                                                                                                                                                                                                                                                              SA;
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 13; 71pp; English
                                                                                                                                                                                                                                                                                                                             Fish
        1017 TCATGGGATATATCATACCTTTCCT
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                     GENESIS RES & DEV CORP LTD.
                                                       ВЪ.
                                                       ADM41470 standard; cDNA; 1083
                                                                                                                                                                                                                                                                                                                             Hall C,
                                                                                                                                                                                                                                                                     09-SEP-2003; 2003WO-NZ000199
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116..901
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                                                                                                                                                                                                                                                                                                                             Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                             2004-248453/23.
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                                                                                                                                                                                                                                      WO2004022700-A2
                                                                                                                                              Lolium perenne
                                                                                      03-JUN-2004
                                                                                                                                                                                                                                                      18-MAR-2004.
                                                                                                                                                                                               sig_peptide
925
                                                                       ADM41470;
                                                                                                                                                                                                                                                                                                                                             WPI;
                                      RESULT 9
ADM41470
                                                              ર્જ
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The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADMA1458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The cryopreservation of a cell or tissue, as a food additive of a frezen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by blocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.

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ADM41462 standard; cDNA; 1084
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                                                                          ADM41462;
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                           RESULT 10
ADM41462
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                                                                                                                          AGGTGGCAGGAGCAACGTCGTGGTCGTGCCACCACGACCTCCACGCGTTGAGGGGCC
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                                                    Gaps
                                                 90;
                           Length 1083;
290 A; 257 C; 262 G; 274 T; 0 U; 0 Other;
                                                 Indels
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                        Score 419; DB
Pred. No. 1.9e-
0; Mismatches
                        42.8%;
llarity 70.4%;
Conservative
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                                     Similarity
 BP;
 Sequence 1083
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The present sequence is that of cDNA encoding AFP3, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a root cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them to the polynucleotides were isolated from tissues taken and ifferent times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold colarance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze colynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                  Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Antifreeze protein AFP3"
                                                                       protein AFP3 cDNA
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WRIGHTSON SEEDS LTD.
                                                                           Perennial ryegrass antifreeze
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1118. .902
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P-PSDB; ADM41475.
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03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                           Key
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A; 258 C; 262 G; 274 T; 0 U; 0 Other; 42.6%; Score 417.4; DB 12; Length 1084; BP.

standard; cDNA; 1064

ADM41465

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CCAGAACTTAATCCATGGCGAAATGTTGGCTGCTGCTCTTCTTGGTGTTCCTCTTGC 105
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                                               CCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGTCTTTGGGGGTTCATCTTGC
                    Gaps
                  90;
   Pred. No. 6e-120;
0; Mismatches 206; Indels
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 70.3%;
                 701; Conservative
Best Local Similarity
Matches 701; Conserv
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The present sequence is that of cDNA encoding AFP4, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADMA1458-ADMA1483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymcleotide, under the control of a gene promocer sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology creagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                         Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                       "Antifreeze protein AFP4"
                                                                                                       Perennial ryegrass antifreeze protein AFP4 cDNA.
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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a basal stem cDNA expression control interaction provides forage grass (peremital ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them fescue) antifreeze proteins and the polymucleotides encoding them at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold cold cold archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the colls of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting cold a natificeeze polypeptide. The antificease protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by blocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient every immurated issue, and to protect a plant from damage due to
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                                                                                                                                                                                                                                                                               Antifreeze;
litholytic;
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                                                                                                                                                                                                                559
                                                                                                                                                                                                                                                                                                              619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCAT 799
                                                                  AGTITICCAGATATTGCTCAAAAGGCTCACCACCGCTGCCGTTCACTGGGTAAGGCGTTC 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGACAAGAAGAATGCCGTATCCGGGGACCACAATACTGTATCTGGAAGCCAAAATACC 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-freeze protein; grass; plant; frozen food product; frost tolerance; frozen confectionery; ss.
                                                                                                                                                                                                                                                                                                                                            472 AACACTGTCATATCCGGGAACAACAACGTCGTGTCCGGGAGCCACAACACGCGTCGTATTT
                                                                                                                                                                                                             ATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCÁACAATGTTGTTTCCGGGAATGAC
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                      AGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGGTTCC
                                                                                                                    ATTAACATGCTATTGCATGTGAGCAGTAG----AAGAACGCTCGATGAAGAACCAAATACA
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confectionery. Anti-freeze proteins are especially used in food products, which are heated, e.g. by pasteurisation, blanching or sterilisation control freezing. Plants transformed with a nucleic acid sequence encoding the anti-freeze protein have an increased frost tolerance. Prior art anti-freeze proteins have not been applied to commercially available code food products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze proteins have tended to destabilise during processing especially during the pasteurisation step. This is overcome by the present anti-freeze protein. The anti-freeze proteins provide an ice particle size following an ice recrystalisation inhibition assay of 15 mu M or less. The anti-freeze protein ingredient can hear mixes can be frozen under quiescent conditions, e.g. in a shop or home freezer without the formation of unacceptable ice crystal shapes and hence with a texture different to products normally obtained via
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 TCTGGAAGCTTCCATACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAATACT 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 27.0%; Score 264.2; DB 2;
Local Similarity 83.8%; Pred. No. 4.4e-72;
hes 299; Conservative 0; Mismatches 58;
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Matches
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T, Briggs SP, Coope
Kreps J, Provart N,
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                                                                                                                                                     ADJ40496 standard; cDNA; 4536
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26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
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KATAGIRI F.
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PROVART N.
RICKE D.
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Goff SA, K
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(RICK/)
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                                                                          В
                                                                                                                                                                                                                                                                                                        The present sequence is that of CDNA encoding APP1, an antifreeze protein of perennial ryegrass. The CDNA was isolated from a pseudostem CDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides controlled in the conding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promocer sequence, into the genome of the organism, or introducing double-stranded CC RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The cutting expression of an antifreeze polypeptide. The cutting expression of an antifreeze polypeptide of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a clisored sistones, to destroy unanted sistones, the dehydrate and kidney stones, to preserve the viability of anotecular biology content, to destroy unanted tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 AAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGGT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCATTAACATGCTATTGCATGTGAGCAGTAG---AAGAACGCTCGATGAAGAACCAAAT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAAT 556
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                                                                                                                                                                                                           reeze proteins and encoding polynucleotides, useful for ig cold tolerance in organisms, as food additives, or for tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAACACGGTCGTATCTGGGGAATAACAACCATGTGTCTGGGAGGAACAACACTGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAACACTGTCATATCCGGGAACAACAACGTGTGTGTGCGGGAGCCACAACACGTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          617 ACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 GTGACTGACAACAAGAATGCCGTATCCGGGACCACAATACTGTATCTGGAAGCCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 262.2; DB 12; Length 841; 73.5%; Pred. No. 3.1e-71; Indels 3; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to protect a plant from damage due to frost or freezing.
                                                                                                                                      Fish SA;
                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1; 71pp; English.
                                                                                         GENESIS RES & DEV CORP
                                                                                                                                    Shenk MA, Hall C,
                             09-SEP-2003; 2003WO-NZ000199.
                                                            2002US-0409557P
                                                                                                                                                                                                           New antifreeze proteins and modulating cold tolerance in
                                                                                                       (WRIG-) WRIGHTSON SEEDS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                      biocrystals (e.g. gout).
                                                                                                                                                                2004-248453/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                              P-PSDB; ADM41471
                                                          09-SEP-2002;
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leaf—and/or stem., panicle, root—or pollen-specific or preferencial or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, eg. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteeins, to incur resistance to insecticides, viruses or fungi, and to
681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to plant nucleotide sequences that direct seed-
                                                                                              797 CATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTGTAGGTG
                                                                                                                                                                  682 AATACGGTATCTGGGAGAAACAATTCCGTATATGGGAACAACAATATTGTATCTG
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rt N, Ricke D,
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cc incur stress tolerance (e.g. salt, cold or drought) to ensure the plants cc have a high nutritional value with reduced apical dominance or dwarfism, cc early flowering or alterated metabolic pathways. This sequence represents a CC plant nucleic acid of the invention. Note: The sequence data for this CC patent did not form part of the printed specification but was obtained in CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html. XX

Sequence 4536 BP; 1102 A; 1247 C; 1221 G; 965 T; 0 U; 1 Other;
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	2;	163	135	220
	6; Gaps	GAGAAC	GGGAAT	TGCTGC
4536;		CTCGCT	TTTGCG	GCCTCA
Length	Indels	TGAGGGG	TGCGGGCA	derceeec
B 12;	86;	ACGCG1	7CGCGC	CCGCAT
8.1%; Score 79.4; DB 12; Length 4536;	Matches 157; Conservative 0; Mismatches 86; Indels	ACCACGACGACCTCC	76 GCTGCGGCGCCCATGCCACCCGGAAGACCTCCTCGCGCTGCGGGGATTTGCGGGGAAT 135	164 CTAAGCGGCAAAGGGGCCGTCCGCGTCGCGCGCGCGCGCGCG
•	vative	STGTCGTGCC	GCGCCATGC	GGCAAAGGAG
ni larit.	Conse	PARCETCO	TGGGGC	rAAGC
tch	157;	104 G	76 G	164 C
Query Match	Matches	ò	Q	Š
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341 TTGGATCTC 349 | || || || 313 CTCGACCTC 321 Search completed: May 11, 2005, 00:27:35 Job time : 657 secs Page Blank (uspto)

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TYPE: DNA
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Sequence 102066,
                                                                                                                                                    May 11, 2005, 01:34:03 ; Search time 704 Seconds (without alignments) 8511.756 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: \cgn2_6/ptodata/1/pubpna/PCT_MBW_PUB.seq:*
4: \cgn2_6/ptodata/1/pubpna/US06_NBW_PUB.seq:*
4: \cgn2_6/ptodata/1/pubpna/US06_NBW_PUB.seq:*
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  5.1.6
Compugen Ltd.
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US-10-260-238-1496
US-10-437-963-4582
US-10-437-963-47843
US-10-027-632-102065
US-10-027-632-102065
US-10-027-632-102065
US-10-027-632-102065
US-10-027-632-102065
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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105088,
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US-10-101-464-861

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US-10-437-953-4738

US-10-425-115-155868

US-10-425-115-155868

US-10-429-933-6767

US-10-719-933-6767

US-10-424-599-138064

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US-10-425-115-3469

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US-10-437-963-39626

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US-10-363-4843-3863

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US-10-437-963-22221

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ALIGNMENTS

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US-10-437-963-77805

US-10-437-963-77805

Sequence 77805, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 77805

MARCH 3285

MARCH 3285
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Pred. No. 2.2e-14;
0; Mismatches 86;
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OTHER INFORMATION: unsure at all n locations
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Best Local Similarity 63.1%;
Matches 157; Conservative (
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US-10-437-963-77805
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196 GCCTGGGACGGCGTCGCCTGCGACGCCGC---CGCCCGAGTCACGGCGCTGCGCCTCCCC 252
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Sequence 4582, Application US/10437963

Publication No. US200401233431

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Application William
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 568, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
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                                                                                                                             341 TTGGATCTC 349
                                                                                                                                                                     313 crccaccrc 321
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ORGANISM: Oryza sativa
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                                              76 GCTGCGGCGGCGCCATGCCACCCGGAAGACCTCCTCGCGCGCTGCGGGCATTTGCGGGGGAAT 135
                                                                                                                               196 GCTIGGGACGCCTIGCGACGCCGC---CGCCCGAGTCACGCCCTIGCGCTCCCC 252
                                                                                                                                                                                                                                                                          281 AAGCGCGCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTAT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AGCTGGGAAGGTGTGGGAAACAGCAAGCGGCCGCGTCGTGGCGTTGCGGCTCCCC 280
                                                                                                                                                                                       221 AGCTGGGAAGGTGTGGGAAACAACAAGGGGCCGCGTCGTGGCGTTGCGGCTTCCCC
                                                                                                   CT---AAGCGGCAAAGGAGCCGTCCGCCTCCGCGCATGGTCCGGCGCCTCATGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: RICKE, DATELL
APPLICANT: RICKE, DATELL
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-4
NUMBER OF SEQ ID NOS: 60/370,620
SEQ ID NO 1496
LENGTH: 4536
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; OTHER INFORMATION: n = any nucleotide
US-10-260-238-1496
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Publication No. US20040016025A1
GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Ricke, Darrell
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Best Local Similarity 63.1
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                            341 TIGGATCIC 349
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APPLICANT: Bradauk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 4582

LENGTH: 2883
281 AAGCGCGCCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTAT 340
                                                     253 GGGCGAGGTCTCGAGGGGCCCATCCCGCCTCCTCGCCGCCCTCGCGCGCCTCCAGGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 CGTGCCACCACGACGACGTCCACGCGTTGAGGGGCCTCGCTGAGACCTAAGCGGGCAAAG 176
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: TONG
FILE REPERENCE: 60111-NP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11452C.1
US-10-437-963-4582
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204 CCGGCGCCTCATGCTGCAGCTGGGAAGGTGTGGGATGCGAAACAGCAAGCGGCCGCGTCG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 CGGCCATCTCGCTGCAGGCCCGCGGGCTCTCCGGGACCCTCCCCGCGGGATCGCCGGGC 271
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                     32 TCCTCCTCCTCGCCGTTCTTGCCGCCGCCTCATCGCGCAACGACGAGGAGGCCCGCGCGC 91
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-22
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-24
PRIOR PLING DATE: 1999-09-28
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Publication No. US20020198371A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50.6; DB 17; Length
Pred. No. 5e-05;
0; Mismatches 154; Indels
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US-10-437-963-47843
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILLING DATE: 2002-09-26
FRIOR APPLICATION NUMBER: US 60/325,448
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2002-04-04
PRIOR PILING DATE: 2002-04-04
SEQ ID NO SEQ ID NOS: 6077
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.2%;
Best Local Similarity 48.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-568
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ORGANISM: Oryza sativa
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LENGTH: 2037
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TYPE: DNA
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OP INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
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                                                                                                   APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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Pred. No. 0.003;
1; Mismatches 112; Indels
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PRIOR PELICATION NUMBER: US 60/218, 006
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102065
LENGTH: 2498
;-10-027-632-102065/c
Sequence 102065, Application US/10027632
Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102066, Application US/10027632
Publication No. US20020198371A1
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Best Local Similarity 51.9°
Matches 123; Conservative
                                                                         GENERAL INFORMATION:
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ORGANISM: Human
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600 GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT 659
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/0218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PAPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-35
PRIOR PILING DATE: 1999-11-36
PRIOR PILING DATE: 1999-11-36
PRIOR PILING DATE: 1999-11-36
PRIOR PILING DATE: 1099-11-36
PRIOR PILING DATE: 1099-10-09-09
PRIOR PILING DATE: 1099-10-09-09
PRIOR PILING DATE: 1099-10-09-09
PRIOR PILING DATE: 1099-10-09-09
PRIOR PILING DATE: 1099-10-09-09
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Pred. No. 0.003;
1; Mismatches 112;
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Pred. No. 0.003;
1; Mismatches 112;
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PLILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 102064, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 51.9
Matches 123; Conservative
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Best Local Similarity 51.99
Matches 123; Conservative
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US-10-027-632-102066
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US-10-027-632-102064
                                                                                                                                                                                                                                     SEQ ID NO 102066
LENGTH: 2498
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Publication No. US20030204075A9
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TITLE OF INVENTION: Identification and Mapping of Single N
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/218,006
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/195,218
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-00-2-24
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
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Matches 123; Conservative
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RESULT 11 US-10-027-632-102066/c ; Sequence 102066, Application US/10027632

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Sequence 79739, Application US/10437963
; Sequence 79739, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rovalic, David K.
; APPLICANT: Shou, Yihua
; APPLICANT: Shoukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF STATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; LENGTH 1614
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR PLILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-04-30
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FBALSEQ for Windows Version 4.0
SEQ ID NO 102066
LENGTH: ANN
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Pred. No. 0.003;
1; Mismatches 112; Indels
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Best Local Similarity 51.9%;
Matches 123; Conservative
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US-10-027-632-102066
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243 TCGGCGGCCCTTCCC 258
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, Publication No. US20(
, GENERAL INFORMATION:
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US-10-437-963-47358
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| Publication No. US20030046728A1
| Publication No. US20030046728A1
| GENERAL INFORMATION:
| APPLICANT: Strabala, Timothy
| APPLICANT: Strabala, Colleen M.
| TITLE OF INVENTION: Compositions Isolated from Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
| TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
| FILE REPERENCE: 1100.1026.2
| CURRENT APPLICATION NUMBER: 09/704,302
| PRIOR FILING DATE: 2002-01-10
| PRIOR PLILOR DATE: 1999-11-01
| PRIOR PLILORATION NUMBER: 60/162,866
| PRIOR FILING DATE: 1999-11-01
| PRIOR APPLICATION NUMBER: 60/162,866
| PRIOR FILING DATE: 2000-01-11
| PRIOR APPLICATION NUMBER: 60/162,866
| PRIOR FILING DATE: 2000-01-11
| PRIOR FILING DATE: 2000-01-11
| NUMBER OF SEQ ID NOS: 989
| SOPTHARE: FRALESCY for Windows Version 4.0
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Pred. No. 0.0059;
0; Mismatches 132; Indels '0;
                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                         Score 44.8; DB 18;
Pred. No. 0.0036;
0; Mismatches 72;
                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_7942C.1
US-10-437-963-79739
                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 48.4%;
Matches 124; Conservative
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                                                                                                                                                                                 Query Match
Best Local Similarity 55.09
Matches 88; Conservative
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -10-101-464A-861
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LENGTH: 3453
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JAPPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Nieuwenhuizen, Nicolaas

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: Compositions Isolated from Plant Cells

FILE REFERENCE: 11000.10203

CURRENT FILING DATE: 2004-06-09

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: PCT/USO0/00724

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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4.6%; Score 44.8; DB 19;
Best Local Similarity 48.4%; Pred. No. 0.0059;
Matches 124; Conservative 0; Mismatches 132;
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Publication No. US20040123343A1
GENERAL INFORMATION:
Application US/10864252
o. US20050050583A1
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APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bucharcv, Andrey A.
APPLICANT: Barbazuk, Brad
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CRGANISM: Eucalyptus grandis
US-10-864-252-861
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123 ACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 ACGACTCCGACATCCTCGCGCTGCTCGAGTTCAAGGATGCCATCGGCGACGATCCGGCGG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TCCGCCTCCGCGCCCCATGGTCCGGCGCCTCATGCTGCAGCTGGGAAGGTGTGCGATGCG 242
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38 -21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 2589
                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%; Score 44.6; DB 18; Length 2589; Best Local Similarity 51.0%; Pred. No. 0.0057; Matches 132; Conservative 0; Mismatches 124; Indels 3;
                                                                                                                                                                                  TYPE: DNA
COGANISM: OFYZa sativa
FEATURE:
CTHER INFORMATION: Clone ID: PAT_MRT4530_50134C.1
US-10-437-963-47358
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NCE 1 (bases 1 to 357)

NSS Jamman, C.D., Sidebottom, C.M., Twigg, S. and Worral, D.

Reezed foods

AL DILLOUR DEFENSION

NULEWER NV

OS Lolium perenne (perennial ryegrass)

PD 12-FEB-2002

PD 12-FEB-2002

PD 23-DEC-1998 GB 9801408.7

PI CARL DUDIEV JARWAN, CHRISTOPHER MICHAEL SIDEBOTTOM, SARAH TWIGG,

PI DAWN WORRALL

PC C12N15/09, A0115/09, A023G9/02, A2313/375, CO7K14/415, C12N15/00 CC

Freezed foods

Freezed foods

Location/Qualifiers

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
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/organism="Lolium perenne"
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/db xref="taxon:4522"
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AK103166 C
AK1032167 E
AL122127 F
AR372178 I
AR972178 I
AC0741677 E
AC126139 F
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AC198103 E
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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AK121984
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CR382398
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Values L. U. 337,)
Sidebottom, C.M.
Direct Submission
Submitted (11-APR-2000) Sidebottom C.M., Plant Science, Unilever
Submitted (11-APR-2000)
Submitted (11-APR-2000)
Submitted (11-APR-2000)
Submitted (11-APR-2000)
Sidebottom C.M., Plant Science, Unilever
Research, Colworth House, Sharnbrook, Bedfordshire, MK44 ILQ,
NNTED KINGDOM
Cds represents presumed mature peptide generated by cleavage before
the first amino acid
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/protein id="CABB7814.1"
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                                                                                                                                                     mRNA linear PLN 29-APR-2000 ice recrystallisation inhibition
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Poeae, Lolium.
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                                 GTTCTTGCTGGGAATGACAACACCGTCATATCTGGGGACAACAATAGTGTGTCTGGGAGC
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    .354
/product="ice recrystallisation inhibition protein"
/note="ORF1"

            GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA
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AJ277399.1 G1:7573547
ice recrystallisation inhibition protein.
Lolium perenne
Lolium perenne
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/note="ORF1"</pre>
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/mol_type="mRNA"
/db_xref="taxon:4522"
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Thesis (1999) University of York
2 (bases 1 to 357)
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Lolium perenne partial mRNA for
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Source
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                                                                                                             RESULT 3
LPE277399
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Frozen food product
Fatent: WO 9937782-A 2 29-JUL-1999;
TWIGG SARAH (GB); UNILEVER PLC (GB); WORRALL DAWN (GB); JARMAN CARL
DUDLEX (GB); SIDEBOTTOM CHRISTOPHER MICHAEL (GB); UNILEVER NV (NL)
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCA 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTG 721
                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                   GTATCTGGGAGCAACCACGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAA 357
                                                                                                                                                                                                                                                                                                                                                                                           GTATCCGGGAGCAACCATATCGGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA 838
GTTCTTGCTGGGAATGACAACACCGTCATATCTGGGGACAACAATAGTGTGTCTGGGAGC
                                                                                                                                                                             121 AACAACACTGTCGTAAGTGGGAATGACAATACCGTAACCGGCAGCAACCATGTCGTATCA
                                                                 GTTGTTTCCGGGAATGACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGAGC
                                                                                                                                                 AACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCA
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                                                                                                                                                                                                                                                                                                             TCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAAT
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Pred. No. 2.4e-60;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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/mol_type="unassigned DNA"
/db xref="taxon:4522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 bp
Sequence 2 from Patent W09937782.
AX019971
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Best Local Similarity 83.8%;
Matches 299; Conservative (
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The:

URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Shishiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FalS Genome Sequencing K. Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T. Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Nau,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Nic,O., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.,
Xie,O., Yokomizo,S., Yoshimura,A., Matsubara,K. Hanagaki,T.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Harao,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Itoh,M., Kagawa,T., Kanagawa,S., Katoh,H., Kouda,M.,
Kishikawa-Hirozane,T., Kanagawa,S., Katoh,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Ota,Y., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Takaki-Akahira,S., Tagawa,A., Takahashi,R.,
Takaki-Akahira,S., Tagawa,A., Takahashi,R.,
Takaki-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Towat, W., Yasunishi,A. and Hayashizaki,Y.
Takaki-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 derecededecedederecedadecedecededecedecedecedecederariadecededada 261
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db x=taxon:39947"
/clone="J033108010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.1%; Score 79.4; DB 8; Length 3392; Best Local Similarity 63.1%; Pred. No. 4.4e-10; Matches 157; Conservative 0; Mismatches 86; Indels 6
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AP004342.5 GI:50510014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Ikeda,R., Sugiyama,A., Mazuno,K., Yokomizo,S., Nikura,J., Rawai,J., Kodama,T., Kowamata,M., Yoshimura,A., Miura,J., Kawai,J., Kawai,J., Kawamata,M., Yoshimura,A., Miura,J., Kawai,J., Carninci,P., Adachi,J., Alazawa,K., RIKERI, Kawai,J., Konno,H., Mayazaki,A., Osato,N., Ota,Y., Saito,R., Saito,R., Shiraki,T., Sobino,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                        AKLZ1984 3392 bp mRNA linear PLN 29-OCT-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033108010, full
insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                              AK121984.1 GI:37991607
FLI_CDNA; CAP trapper.
Oryza estiva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba; Ibaraki
                                           838
                                                                       301 GTATCTGGGAGCAACCACGTTGTATCTGGAAGCAACAAAAGTCGTGACAGACGCTTAA 357
                                   GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   japonica rice
Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 3392)
Kikuchi, S.
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Unpublished
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JOURNAL PUBMED REFERENCE AUTHORS

TITLE

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REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

TITLE

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ASTGVFELDVVYTTPNATTIDASAPVSPLDGGGSSGSTSTAKSGAAGRQVGWVSACVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mavtgvgvlgdgggwrwwgcasrtwnrisgggdtlllwsrwve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-coding transcript
probably inactive due to including stop codon(s) in CDS"
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protein related/dirigent protein-related"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P055H11.106"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (8221. .8754)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Augrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasakianias affer.go.jp, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, URL: http://rgp.dna.affer.go.jp/, GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://rgp.dna.affer.go.jp/RiceHMM/), SplicePredictor (http://www.tigr.org/software/glimmerm/), BinASTN and BlaSTX. The genomic sequence was searched against NCBI NonRedundant Protein database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with blaSTR. ESTS represent the identified cDNA sequences using BlaSTN with the corresponding DDBJ accession no. and RGP clone ID. Pull-length cDNAs represent the identified cDNA sequences using BlaSTN with the corresponding DDBJ accession no. and RGP clone ID. BlaSTN with the corresponding DDBJ accession no. and RGP clone Such as seme name, 'putative.' and 'like protein.' A gene without significant homology to any protein name to indicate the homology to any protein but with full-length cDNAs represent the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by a single gene prediction program is classified as an 'unknown' protein. A gene predicted by a single gene prediction program is also classified as a miscellaneous feature of the sequence is feature of the sequence is december of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0585H11 clone has an overlap with B1317D11 (DDBJ. AP006186) clone at 5' end and with OJ1567 (DDBJ. AP003759) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.ip/GenomesSeq.html.
                           Oryza sativa (japonica cultivar-group)
Wakaryota, Viridplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-NOV-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                             Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0585H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                                                                                              T., Matsumoto, T. and Yamamoto, K. Submission
      (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                 Published Only in Database (2001)
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                                                                                                                                                                                                                                                                                                                                (bases 1 to 149371)
                                                                                                                                                                                                                                                                                                                                                                  Sasaki, T
SOURCE
                                                                                                                                                          REFERENCE
AUTHORS
TITLE
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Eukaryota, Allendari Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alvocidata; Apicomplexa; Haemosporida; Plasmodium.

(E 1 (bases 1 to 349418)

RS Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C. O., Burrows, C., Cherevach, I., Chillingworth, C., Christodoulou, Z., Clark, L., Clark, L., Clark, L., Cark, R., Corton, C., Chillingworth, T., Goble, A., Goodhead, I., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Monsey, T., Holroyd, S., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Harper, D., Haughray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Knnfortov, B., Kyes, S., Larke, N., Karbornou, A., Knights, A., Knnfortov, B., Kyes, S., Larke, N., Rabbinowitsch, E., Rajandream, M., McLean, J., Mooney, P., Rabbinowitsch, E., Rajandream, M., Sumonds, M., Seger, K., Sharp, S., Smtth, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Squares, S., Sevens, K., Taylor, K., Tivey, A., Unwin, L., Squares, S., Sevens, K., Taylor, K., Tivey, A., Unwin, L., Squares, S., Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13

L. Nature 419 (6906), 527-531 (2002)
                   349418 bp DNA linear INV 30-MAR-2004
Plasmodium falciparum chromosome 6, complete sequence; segment 1/5.
CR382398 1 GI:46362238
HTG.
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
Barrell, B.G.
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus,
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4 (bases 1 to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berry, A.B., Berriman, M., RA Pain, A., Hall, N., Atkin, R.,
Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R.,
Hall, S., Quail, M. and Barrell, B.G.
Direct Submission
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/locus_tag="PF0005c"
/note="WAL6Pl.317"
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/isolate="3D7"
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/gene="VAR pseudogene"
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3D7
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                                                                                                                                                                                                         Plasmodium falciparum
Plasmodium falciparum
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                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                      RESULT 6
CR382398/c
                                                                                                                                                                                                                                  ORGANISM
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MEDLINE
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REFERENCE
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AUTHORS
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GGTGAPRMATGVVLWRTASWQPRADAVLELDVFVHTRPEYLQSPPPPHHRPPPPTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AGCTGGGAAGGTGTGGGATGCGAAACAGCAGCGGCCGCGTCGTGGGCGTTGCGGCTCCCC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains EST(s): AU056601(S20723),AU056602(S20723)
contains full-length cDNA(s): AK064359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26336 GCTGCGGCGCCGTGCCACCCGGAAGACCTCCTCGCGCTGCGGGCATTTGCGGGGAAT
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Pred. No. 8.9e-10;
0; Mismatches 86; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compress #10585H11.108"

complement (join(<20109. .20350,20514. .>20613))
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/note="start and end point are not identified"
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'gene="P0585H11.107"
'note="start and end point are not identified"
join(15804. .15851,16016. .16324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="start and end point are not identified"
26261. .29293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join(20109, .20350,20514, .20613))
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/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative phytosulfokine receptor" /protein_id="BAC20742.1"
                                                                                                                                                                                                                                                                                                                                                'note="predicted by GENSCAN etc."
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<26261. .>29293
/gene="P0585H11.109"
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Matches 157; Conservative
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LGIYYEKLENLFKSNFPQVMKALEGDEKGKWYQFKDDLKKKFEFESEKNTRTTDSQDAI
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MMDNETGMKHAKKHLKDVFDNIRKSLKONGLNDLKDKETYCRAMKYSFADLGDIIRGRD
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KENSENDENDENNYYKOKOPOGEILGILCPNKKIDKOKKEILDETSSKFR
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MCALTNOLTDDEKKOBL TYKXS YDEDSSLEEFFORTSQFLEWWTEWEG
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TYLDYVPQFLRWFDEWSEEFCRKRNITLKSAKEECQNDSKKLYCSLNGYNCTRLIPNK
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LYSGEEYSYNVMMVNSMDDIPINRDNNVYSGIDLINDTLSGNKHIDIYDEVLKRKENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWENETHSGNTHPSDSNKTLNTDVSIQIHMDNPKPINQFTNMDTILEDLEKYNEPYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNNNDVGACAPFREHLCDYNLEKMGSTKIKDKNVLLAEVCMAAKYEGQSLLKQYEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNNYPHTNICTVLARSPADIGDIVRGKDLFLGHQQRKRKLEENLKQMFENIKKANDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEDTSHVQPPPLPPKPSTPEVEPLPSDEPFDPTILQTT1PPGVALALGSIAFLFLKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLSPVDLFSVINI PKGDYNI PTLKSSNRY I PYASDRYKGKTY I YMEGDSSGDEKYAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDTTDITSSESEYEELDINDIYVPRAPKYKTLIEVVLEPSKSNGNTLGDDIPHTNKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFGTNHTKKNTSTNSVAKNTNSDP1LNQINLFHTWLDRHRDMCEKLKNDNERLAKLKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQDDIYYDVNDHDASTVDSNAVNVPSKVQIEMDVNTKLVKEKYPIADVWDI"
complement(join(15065, .16126,16357, .16410))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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db_xref="GI:46362239"
'codon_start=1
'product="erythrocyte membrane protein 1 (PfEMP1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (15065. .16126,16357. .16410))
                                                                                                                  db_xref="PSEUDO:CAG25172.1"
|oin (3503. .10936,11630. .12835)
|gene="VAR"
                                                                                                                                                                                                                                                                                   уолп(3503. .10936,11630. .12835)
gene="VAR"
                                                                                                                                                                                                                                                           locus tag="PFF0010w" oin(3503, 10934, 1167
                                                                                                                                                                                                                                                                                                                                                                                                          locus_tag="PFF0010w"
note="MAL6P1.316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus tag="PFF0015c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tag="PFF0015c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MAL6P1.315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="RIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus
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273255
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                                                                                                                                                                AINWWKTTEIAÄATKÄAIAAGKAAGKIAGEAAGKKAVIEALKYFGVDDFFPEIFKSIL
KORNYTDYTKEGALIAEKHVINCANSARGSSVNDSTCNAFEIKLGIJEAETGKPNGPP
AYQAIPQKINELAEEATQAARAAKKAKSESATAAFETAEKEAIEASMQLYTTIAYSI
LAILIIVIMVIIVILRYRRKKKKKLOYIKLIEE
COMDIEMENT (join (18586. 19821,19980. .22721))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFSQCKLLGKKY SNYSNEATEAMKESYADYSDIVKGTDMMDLKKLNKELNTLLKETE
MAQDY CKEKLLGKKY SNYSNEATEAMKESYADYSDIVKGTDMMDLKKLNKELNTLLKETE
MAQDY CKEKLL KRAHI INTKKOI VEGREKHKSMVD ITDVECKRLP IDYEBMFRYRYNGM
KGGLSRYT KKTKKRSGVNI PSEECAASYTYKHCNGCI CNILADMED HKNINNONELM
KEMINI I KFDTDQYRTQLQNI SNSMEINPKSVKTAVDTTKDIVSYGLAGTMGVAAIGL
GAGDFLGKKY CDLYNBEPMKPEKKLDTSSKNLNI YBEDPNIMPSAGIGYALTGLILFK
MRRKAKQVUMI RILLQMSQNSYGI PTTKSPNKYVPYGSQRYKGKTYLYVGGTDEKY
MRRKAKQVUMI RILLQMSQNSYGI PTTKSPNKYVPYGSQRYKGKTYLYVGGTDERY
MRRKAKQVUMI RILLQMSQNSYGI PTTKSPNKYVPYGSQRYKGKTYLYVGGTDERY
                                                                                                 YAPATYDDDPQMKEVMQQFEDRTSQRFHEYDERMKTTRQKCKDKCDKE1QK111KDKL
EKELMDKFATLQTD1QNDA1PTCVCEKSLEDKMEKGCLRCGGVLGGG1APTFG11GSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EADGIGISSLILPYSKCGRDTDPPVVDYIPQRLRWMSEWSEYFCNVLNKEIDEMNNQC
KDCEMSRRCNNDTEGEKCKKCKEQCQIFKELVSKWKNEFDKQSMKYKELYIKASTNIT
KQNSSSPERGYRRNHRRRGYDDDTNVQLFLKKVIENNECKVESLGKYLDKTSHCGNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="G1:46362241"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVLVTAKYEGDYI VNNHPNRGSSEVCIALARSFADIGDI VRGKDMFKSNDNVENGLRE
VFKKIYEGFLDKGAREHYKEVKNGNYIKLREDWWTANRDQVWKAMTCVAPENAYFRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNYDNI PGSNR PNA PEI PPEKPKKA CKCKI PNPLEKCPNEENKNYCTR PDKYSS CTSL
PFKNDLI EWNNSGVKNKENDNNGYL VPPRRRNLCI NLFSKKDY KMKDENDFKEDLLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKLIDEEWNQLKDDFISQYLPNTEPNNNYRSGNSPINTNNTTTSHDNMGEKPFIMSIH
DRNLYTGEEISYNINMSINTNNDIPKYVSNNVYSGIDLINDTLSGNKHIDIYDEVLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KENELFGTNHVKQTSIHSVAKNTYSDDAITNKINLFHKWLYRHRDMCEKWENHHERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKEKWENDNDGGNVPSDNHVLNTDVSIEIDMDNPKPINQFSNMDINVDTPTMBDNMED
DIYYDVNDNDDDNDQPSVYDIPMDHNKVDVDVPKKVHIEMKILNNTSNGSLEQQFPIS
                                                                         translation="MKIHYINILLFELPLNILIYNQRNHNSTTPHHPPNTRLLCECEI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ONR FDENAEAYCNSDK I RGNENNSNAGACAP FRRONLCDKNLEYL I NENTKTTHDLLC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="erythrocyte membrane protein 1 (PfEMP1)-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579 ATAACAACCATGTGTGTGTGGGAGCAACACACTGTTGTAACTGGAAGTGACAATACTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273374 ATAACAACAATATGGTGGATGATAACAACAATATGGTGGATGATAGCAACAATATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273314 ATGATAACAACAATATGGTGGATGATAACAACAATATGGTGGATGATAACAACAATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 TIGGTAGCAACCATGICGTATCAGGGACAAAGCATATTGTTACTGATAACAATAATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus tag="PPF0020c"
/note="Does not produce Pfam hit to PFEMP domain
(pfam:PF03011), found in Pfempl protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="PFF0020c"
complement(join(18586. .19821,19980. .22721))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 349418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus tag="PFF0025w"
join(26557. .26610,26766. .27830)
/gone="RIPP0025w"
/locus tag="PFF0025w"
/note="MAL6P1.313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(26557. .26610,26766. .27830)
/gene="RIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 76; DB 3; 55.8%; Pred. No. 8.7e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
/protein_id="CAG25174.1"
/db_xref="GI:46362240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'protein_id="CAG25175.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           possible pseudogene
MAL6P1.314"
                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="VAR-like"
                                                                                                                                                                                                                                                                                                                                        gene="VAR-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Simi
hes 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                            gene
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UKL : http://canal.rana.atrrc.go.jp/cubn.

UKL : http://canal.rana.atrrc.go.jp/cubn.

NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,

Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,

Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T.,

Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and

Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,

Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,

Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,

Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,

Sugiyama,A., Suzuki,Y., Tsunoda,Y., Uoda,M., Ryu,R., Sugano,S.,

Sugiyama,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center

and Genome Stonce Laboratory in Riken: Adachi,J., Atama,A.,

Akimura,T., Arakawa,T., Carninci,P., Pukuda,S., Hanagaki,T.,

Akimura,T., Arakawa,T., Carninci,P., Pukuda,S., Haradayi,Y.,

Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,

Kishikawa-Hirozane,T. Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Muyazaki,R., Ohno,M.,

Ota,Y., Saitch,H., Sakai,C., Sakai,K., Sakazume,N., Naki,K.,

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Takahashi,F.,

Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,

Yasunishi,A. and Hayashizaki,Y.

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
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F1LCDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Guyza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 CGGGTAATTCATTGGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGAGCCTCA 410
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/mol type="mRNA"
/culfivar="Nipponhare"
/db xref= traxon: 39947"
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Pred. No. 7.1e-09;
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Best Local Similarity 68.4%; Pred. No. 7.1e
Matches 119; Conservative 0; Mismatches
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                                                                                                                     273194 TGGTGGATGATAACAACAATATGGTGGATGATAACAACAATATGGTGGATAATCACAATA 273135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) cDNA clone:002-108-B08, full insert sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptrophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                        CCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGGAGCAACA
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Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakawi, K., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawanata, M., Matsubara, K., RIKEN: Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Yoshino, M., and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, K., Shinagawa, A., Shiraki, T., Yoshino, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashizaki, Y., Hayasusu, N., Hiramoto, K., Hiraoka, T., Hayashizaki, Y., Hayasusu, N., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, J., Ikayasusu, R., Imamura, K., Imamura, K., Imahiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koda, S., Kurlahara, C., Kurosaki, T., Mushmegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Myazaki, A., Maniki, T., Narikawa, K., Murata, M., Nagata, T., Mamura, M., Namaski, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Suzuki, T., Tagami, M., Tagami, Takeda, Y., Tawahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yotom, P., Lanka, J., Yazaki, J., Yokomizo, S. and P., Lanka, L., Lanka, L., Lanka, L., Yazaki, J., Yokomizo, S. and P., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Yazaki, J., Yazaki, J., Yokomizo, S. and P., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L., Lanka, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Head of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological. Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp, Tel:81-29-838-7007, Fex:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        japonica rice
Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2958)
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JOURNAL
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COMMENT

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CNSOBCBF
Human chromosome 14 DNA sequence BAC R-731F5 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1085 CAAACAATTCCTTAGTCGGCGAGATACCGAAGAGTTT---GACGCAGCTCAAGAGCCTTG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 CGGGTAATTCATTGGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Holis, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-SEP-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                   TTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1025 TGGTTGGCACCATCCCTGAATGGATCGGTCAACTTGATAACCTGACCTACTTGGATCTTT
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1142 TCACCGCCCGACGTTCGCCGGGTATGGCGTTCACTAACATGCCGTTGTATGTGA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464
                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:3994"
/clone="U033121E13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 24, 2002 this sequence version replaced gi:23306222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap, version 2.0 Quality coverage: 11.37x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 CCACTGACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGA
                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                     Length 2958;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the T7
                                                                                                                                                                                                                                                                                  Score 74.8; DB 8;
Pred. No. 7.5e-09;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The following sequence is oriented fractions.—— Finitabing boundaries FINISHED SEGMENT STARTS AT BASE 1 FINISHED SEGMENT ENDS AT BASE 124850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
1. .2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL928742.3 GI:23306225
                                                                                                                                                                                                                                                                               7.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Homo sapiens (human)
Homo sapiens
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55713
56253
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                                                                                                                                                                                                                                                                    Unpublished
                CNS01DT2
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220
330
440
400
90
                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                 LOCUS
DEFINITION
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                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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   CNS01DT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7724 CAGGAAGCATCCAGAGTGGAACAGGAAATGTCCAGCATGGAACAGGAAGCATCAAGAATG 7665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7664 TAACAGGAAGCATCCAGAGTGGAACAGGAAATGTCCAGGATGGAACAGGAAGCATCCAGA 7605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 TGTCTGGAAGCTTCCATACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAATA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             dbSTS:STS21065
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                        dbSTS:ST548887
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dbsTS:STS56700
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dbsrs:srs41544
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schuler) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7604 ATGTAACAGGAAGCATCCAGCATGGAACAGGAAGCATCCAGAGTGGAACA 7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%; Score 70.2; DB 9; Length 176237; Best Local Similarity 56.5%; Pred. No. 2.8e-07; Matches 130; Conservative 0; Mismatches 100; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780 CTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACA 829
                                                                                                                                                            >= 40 : 99 %.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identified using the e-PCR software (G.
                                                                                                                                                        Percentage of bases with a quality value Location/Qualifiers 1. .176237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158529. .158653
/note="matching EMBL:AA160692
                                                                                                                                                                                                                                                                                                                                                                            57606. .57752 /note="matching EMBL:L00022
                                                                                                                                                                                                                                                                                                                                                                                                                                                        60040. .60260
/note="matching EMBL:M55420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145938. .146060
/note="matching EMBL:Z53040
RHdb:RH9751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69316. .69421
/note="matching EMBL:H26187
                                                                                                                                                                                                                                                                                                                 'note="matching EMBL:G14654
                                                                                                                                                                                                      organism="Homo sapiens"
/mol type="genomic DNA"
                                                                                                                                                                                                                 /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                     clone="R-731F5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dbsrs:srs37918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dbsrs:srs5550
                                                                                                                                                                                                                                                                                                   .14567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHdb: RH80278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHdb: RH48485
                                                                                                                                                                                                                                                                                                                                                                                                              2Hdb:RH68981
                                                                                                                                                                                                                                                                                                                                   2Hdb:RH7974
                                                                                                           54448
79950
110 - 12
220 - 29
440 - 139
550 - 59
60 - 69
90 - 89
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RESULT 10

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CNS01DT2 169802 bp DNA linear PRI 19-NOV-2001 Human chromosome 14 DNA sequence BAC R-417P24 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
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Direct Submitssion
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
Submitted (19-NOV-2001) Genoscope :
Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 169802)
1 (Bases 1 to 1.0.1. Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Ekcheberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The following BAC sequence is oriented from the T7 to the SP6 end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Nov 20, 2001 this sequence version replaced gi:14715169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identified using the e-PCR software (G. Schuler)" 39191. .39405
/note="matching EMBL:G33053
RHdb:RH67749
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Identified using the e-PCR software (G. Schuler)"
11439. .11536
/note="matching EMBL:G14654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percentage of bases with a quality value >= 40 : 99 %.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Genoscope / Centre National de Sequencage
Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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/note="matching EMBL:G33053
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/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="R-417P24"
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Range : bases
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                                                                                                AL122127
AL122127.6 GI:17026193
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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bucke, C.O., Burrows, C., Chaerevorh, T., Chillingworth, T. Chistodoulou, Z., Clark, L., Clark, R., Corton, C., Cholin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, T., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Karhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Line, A., Modlean, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Suttherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
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                                                                                                                                                                                                                                                                                          /protein id="AAL25757.1"
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/db xref="G1:16551243"
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YKTREDEXGTLEEDSEERYGTLEEDSKETLEEDSYGTLEEGYGSPENRYKTREERY
GTXEEDSEDSESESEKSGTLEEDSEEDSEDSEDSESTGSPERSTLIKKEGFIEHRGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AAGAATATCGTACCCAAGAGAAGAATATCGTACCCAAGAGAAGAATATCGTACCCAAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725 GGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AAGAGGAAGAATATTGGACCCGAGAGGAAGAGTATAGGACCCGAGAGGAAGAATATAGGA 271
                                                                                                                                             /note="grass-specific insert; similar to Oryza sativa sequence deposited with GenBank Accession Number X15901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamlin, N., Pain, A., Berriman, B., Hall, N., Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                 polymerase beta' subunit 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665 ACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 AACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGG
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAAGAGAAGAATATCGTACCCAAGAGAAAGAATATAAGACCCGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%; Score 63.8; DB 8; 1
llarity 55.1%; Pred. No. 5.4e-06;
Conservative 0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                        /codon_start=1
/transT_table=11
/product="DNA-directed_RNA_1
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Plasmodium falciparum MAL4P1.
AL034557 AL844503
AL034557.8 GI:23498126
                            <1. . . >646
/gene="rpoC2"
                                                                                                                gene="rpoC2"
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                                                                                 .>646
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Best Local Simi
Matches 125;
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ACCESSION
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                            gene
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AUTHORS
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JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
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SOURCE
                                                                                    CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19473 ACAGGAAGCATGCAGAGTGGAACAGGAAACGTCCACCATGGAACAGGAAGCATCCAGAGT 19532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19533 GGAACAGGAAGCATGCAGAGTGGAACAGGAAATGTCCAGCATGGAACAGGAAGCATCCAG 19592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF372178 646 bp DNA linear PLN 18-JUN-2002 Leptocoryphium lanatum DNA-directed RNA polymerase beta' subunit 2 (rpoC2) gene, partial cds; chloroplast gene for chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Paniceae, Leptocoryphium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCAACAACACCTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          659 TCAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19593 CATGGAACAGGAAGCATCCAGCATGGAACAGGGAGCATCCAGAGTGGAACAG 19644
                                                                                                                                                                                                                                                                                    dbSTS:STS51071
Identified using the e-PCR software (G. Schuler)"
131895. .132128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779 ACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAG 830
                  (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                   identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHdb RH51956
dbSTS:STS23199
Identified using the e-PCR software (G. Schuler)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 169802;
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Direct Submission
Submitted (18-APR-2001) Biological Sciences, Northe University, Montegomery Hall, DeKalb, IL 60115, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 103; Indels
            1. .646
. Organism="Leptocoryphium lanatum"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67.2; DB 9;
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phylogenetics of Paniceae (Poaceae)
Am. J. Bot. 88 (11), 1988-1992 (2001)
2 (bases 1 to 646)
                                                                                                                                                                                            39281. .39447
/note="matching EMBL:X99549
                                                                                                                                                                                                                                                                                                                                                                                     note="matching EMBL:X00253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="matching EMBL:R05773
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Duvall,M.R., Noll,J.D. and Minn,A.H.
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                                                                                                                                          dbSTS:STS21065
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                                                                                                                                                                                                                                                                                                                                                                                                                                          dbSTS:STS3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%;
                                                                                                                                                                                                                                                              RHdb: RH71306
                                                                                                                                                                                                                                                                                                                                                                                                              RHdb: RH18069
                                                                                                             RHdb:RH7974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local S
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VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
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AUTHORS
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FEATURES

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Direct Submission
Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Gasgdaknyiddlkgdlokapninpkiigtddpcklyedyynnhyngdgkgerypcte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YESARREKLENKLKEVFGKIHGGLSEBAKKKYODGDGNYYQLREDWWTANRETVWKAI
TCEVKSGNNYFRATCGDEKNPSLTSKQCRCDKDKAGKPIKGSGNVNIVPTYFDYVPQY
LRWPEEWAEDFCRLRKHKLKDAIKKCRGKNGEEKYCDLNRYDCKNTASGKHVFFEDFD
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TFYRTKYCEACPWCGAEKVEGGWKAKEENCSQTKDYDPDKTTTIEILTGDTRKSDMVQ
KYKKFCNGNGGNGEKSATPNATSREKGKKGDQMEKWICYYDENKEKKYGSDAINFCVL
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EKGLDAEEAKEIKHLROMLEQAGVRDLAAVGGPCTEGGVAEQNTIMDKFLDEELKEAE
OCKNCPKPKAQQEGPGGARSADSPPAGTEDHPDAEDDDDEDDDDDDDDEDEEEEEEED
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YYIAHESETKNIETQDDLRDAFIRTAAAETFLSWQYYKIKNGADAKQLDNGTIPEEFL
RSMYFTYGDYRDICLNTDISKTVNDVAKAKDKIGKFFSKDGSKSPSGTTTPQDWWQTY
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WRGBERCABERGKLEQDIGGSCNGINP LQYCSDPNPCKNFCOEPTKQNFTKQKERRGQ
TTKEVRDANLENADGSYKDYKTYGPSKGONDYLNDKODNKKCSGMEGNVLTDVSSKK
PRGI YAHKYSEKCNCLGAKFVPTNVPPAPPPQPPPPALPAPATPGVNPCEI VNTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDTNKFKDACTLKYGPKAPTSWKCIPTGNTSNEGAATDSEGSDAKSRHKRDLAPSSGS
NQGSICVPPRRRKLYVTPLTKWAEETTKGSKSQESGKAEGTSESSGSEASSPGGTSSQ
GEKSPQGLSTPASTSSPSNSRDDDLLKAFVESAAVETPFLWHKYKMDKQKELDEKKKQ
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SSLTRETLWKEHAPSIWEGMICALTYKENDEKKIVKONEVYEKPFGTTPGTTSGKYKE
KYEYNTVKLDENSDTEAKDTKATAPSONTPTFLSHFVLRPPYFRYLEBWGETFCKERK
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NTTASGNNTTASGKNTPSDTQNDIQSDGIPSSKITDNEWNTLKDEFISQYIQSEQPKD
VPNDYSSGDIPFNTQHNTLYPDKPDEKPFITSIHDRNLYTGEEVNYDMSTNSGNNDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to Plasmodium falciparum variant-specific
surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa)
fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
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KKI EFGEQKSAYVKQKTKCKEESGGGGNGVCGTVKTCDTAAQFLERLGPCKNNDNGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIEFNEQSETFKHTKHCDPCSSFKIDCRNGKCKSGDTKGKCDGITTIDAKEIAKMISS
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KKKTKSTIDLLRVINIPKSDYDIPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLEVCMAAKYEGOSINTHYTKHEHSNKDSPSQLCTVLARSFADIGDIVRGKDLFYGNT
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                                                                                                                      CBIO 1SA, UK
ON Oct 3, 2002 this sequence version replaced gi:5731897.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
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/db_xref="G0A:081220"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Join (35153. .41725,42757. .44124)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                         source
    TITLE
JOURNAL
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DKERLYCSQNOYDCTRRIEKGSSCSRENKCTGCSNKCYDYDFWLEKQNEFKIQKDKY
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gene

CDS

/mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN

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233583 GTTATTACAATATTGTTCATGGTTATTATATATTGTTCAGGGTTATTACAATATTGTTC 233642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233582
                                                                                                              WLQTWKEHYEKQKI KYENDKDSYTNDPDTKQSPQAYQYLANKKLEKI CPSGNTSANCEY
KCKYEYSSQNNNNMPAALDDTBOJYKTOTCKTKSQASSNEWSKREBDEBGDPPPRAPRAP
RQSLAKSANNPSPRAPPGGGPPDAGGARAETGPSPQQPPRFPAALL
QPLAKVDQDEEEDBEDDEEBDGESGSEEGGGDVDDSDSSEDENDEEDBDDSHHVVDGH
                                                                                                                                                                                                                                                                  QBEBPPDETEVVBETVAAPEVKPACEIVKELFNDTNKKFKDACNLKYGGNNSRLGWKCI
PSGDSTTTSSYNGDRSQRHRRAAGEATGKSDASGSICVPPRRRLYVGKLTQWASQRY
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ETFAKRPQFLRWFTEWGDEFCREQKKQLDILKKKCPKETCTNEGKKKECSDACKAYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKYQGELDKI.NGNSNGNNNCCKEIKKGTSASEFIKELKHCKDGONSEDTDKSEEDKK
NNKIDPNKPLETFNPSTYCETCPSNKVNCNGSGRGTRGKDPCTPHNEKGKSWESVPNA
DLQNQLESGIIPDDFKRQMFYTFGDYRDFLFGTDISKGHGIGSELAKKIDSLFKNIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENSGAKPTQPPSPSGDNTPTTLTNFISRPPYFRYLEEWGETFCRERKKRLEEVRKECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEYPGEKYCGGDGHDCTENGELKHTNMFADLDCRDCHKQCRKYRKWIDIKFEEYEKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGGNSTEITVEMIDRREPLIKNYSKILEESGNSSDSLFKTSRLFKSVRDQQWECRYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTDI CKLKNFNDKI DLAQYTTFKVFLEYWLQDFI EGYY ILKKRKI I EQCKENGGETC
NENSKNDCACVKGWVAQKTTEWNQI KDHYNKKEYGNGYDMSHKVKNY FEKNENELRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 ATGTTGTTTCCGGGAATGACAACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233523 ATTTATATTATATGAATGATTACTTTGTTGAATATTATTGTTTTATAATATTGTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%; Score 63.8; DB 3; Length 347582; llarity 50.5%; Pred. No. 1.8e-05; Conservative 0; Mismatches 152; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .<u>`</u>
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Matches 155;
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L (Dases I to 2618)

I (Dases I to 2618)

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Barder, W., Barder, E., Baden, H., Barderanaike, D., Barber, M., Barastaad, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barnstaad, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brado, S., Brach, T., Censar, H., Center, A., Carder, K., Carder, K., Carder, K., Carder, M., Charder, C., Cockrell, R., Cock. Coyle, M., Chen, Z., Chu, J., Charda, C., Cockrell, R., Cox., Coyle, M., Chen, Z., Chu, J., Davis, C., Davalla, M., Davis, C., Davalla, T., Pan, G., Davala, M., Eugene, C., Evans, C.A., Palla, T., Fan, G., Pagan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, M., Garcia, M., Garra, M., Gabregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gabsegoorgis, R., Haaland, M., Hamil, C., Hamilton, K., Harnandez, R., Haaland, W., Hamil, C., Hamilton, K., Harnandez, R., Haches, S., Hlawe, A., Henderson, N., Hernandez, J., Howells, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Hulyk, S., Khan, Z., Kopis, L., Lobow, H., Levan, J., Lu, X., Ma, J., Lu, X., Mangum, R., Maheshwai, L., Loulseged, H., Lozado, R., Lu, X., Marin, S., Marten, S., Marten, S., Marten, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus clone CH230-104014, WORKING DRAFT SEQUENCE, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GAGTGGAACAGGAAACGTCCACCATGGAACAGGAAGCATCCAGAGTGGAACAGGAAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         733 CCATACTGTATCAGGGGAGCACACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAG
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                                                                                                                     Gaps
                                                                                                                     ;
           Length 300;
                                                                                                                     Indels
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Rattus norvegicus (Norway rat)
Rattus norvegicus
     Score 62.8; DB 6;
Pred. No. 8.7e-06;
0; Mismatches 97;
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AC126139.7 GI:30520607
6.4%; 8
milarity 55.5%; E
Conservative 0;
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                                                             Similarity
                                                                                                                Matches 121;
                                                                                                                                                                                                                          613
           Query Match
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AC126139/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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PAT 03-FEB-2004

linear

CO741677 300 bp DNA Sequence 27611 from Patent WO02068579.

CQ741677 CQ741677

DEFINITION RESULT 13 CQ741677

CQ741677.1 GI:42350302 Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens

REFERENCE AUTHORS TITLE

Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses

thereof Patent: WO 02068579-A 27611 06-SEP-2002; PE Corporation (NY) (US)

JOURNAL FEATURES

Corporation (NY) (US) Location/Qualifiers

source

/organism="Homo sapiens"

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                 source
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24819414.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.mc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, T., Thomas, N., Thingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walliams, G., Willsans, S., Warren, R., Wei, X., White, F., Williams, G., Willsan, S., Yen, J., Yoon, L., Yoon, V., Widerhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 261587).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Atlas 3.0;
Consensus quality: 245312 bases at least Q40
Consensus quality: 249138 bases at least Q30
Consensus quality: 252151 bases at least Q20
Estimated insert size: 257796; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250010: contig of 250010 bp in length
250110: gap of unknown length
253467: contig of 3357 bp in length
253567: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center project name: GHUJ
Center clone name: CH230-104014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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TITLE
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Rattus norvegicus clone CH230-462N7, WORKING DRAFT SEQUENCE.
AC119701
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83753 ATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTTTGTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 TCTGGGAATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83693 T-----Grancagcacricitraacarcrarcagcacriciteracarcrarcagcacr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83579 ACTGTTGTAGCATGTATCAGCACTGTGTTAACATGTATCAGCACTGTTGTAGCATGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              752 CACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 AACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.2%; Score 60.8; DB 2; Length 261587; Best Local Similarity 51.9%; Pred. No. 0.00011; Matches 165; Conservative 0; Mismatches 147; Indels 6;
255148: contig of 1581 bp in length
19 255248: gap of unknown length
9 256807: contig of 1559 bp in length
8 256907: gap of unknown length
5 25868: contig of 1678 bp in length
5 25868: gap of unknown length
260166: contig of 1481 bp in length
260266: gap of unknown length
261587: contig of 177
                                                                                                                                                                                                                                                     7 261587: contig of 1321 bp in length.
Location/Qualifiers
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260167
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RS MIGNESS I to 172927)

RIGHGROUND C. Allen, "Albabrooks, S., Amin, A., Angulano, D., Allen, "Albabrooks, S., Amin, A., Angulano, D., Allen, "Albabrooks, S., Amin, A., Angulano, D., Allen, "Albabrooks, S., Amin, A., Angulano, D., Bandaranaike, D. Bander, "Barder, M., Barnstead, M., Benahmed, F., Baldarin, D., Bandaranaike, D., Bander, S., Barnstead, M., Benahmed, F., Baldarin, D., Bandaranaike, D., Earber, M., Barnstead, M., Benahmed, F., Baldarin, D., Bandaranaike, D., Chen, S., Chen, R., Chen, S., Chu, J., Chen, S., Chen, R., Chen, T., Chen, T., Chardon, S., Chen, R., Chen, R., Chen, T., Chen, T., Chardon, D., Chen, C., Chen, R., Chen, T., Chen, T., Chardon, D., Depard, C., Covetell, R., Cox, C., Coyle, M., Cree, A., Deferer, A., Depard, M., Dugan, Roche, S., Durny, Carroll, L., Dand, B., Baves, K., Ban, G., Friney, M., Flaggn, N., Porbes, L., Foster, M., Gaverra, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Guevara, M., Mandara, E., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., March, M., Morris, S., Park, K., Morris, S., Park, K., Morris, S., Park, K., Morris, S., Park, K., Perez, L., Senater, M., Savart, G., Selendon, J., Steretto, J., Sandor, M., Savart, G., Selendon, J., Steretto, J., Sandor, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

Baylor Plaza, Houston, TX 77030, USA.

The sequence in this sequence version replaced gi:23908282.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using ARlass (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly a "contigs scaffold"). Within each contigs casffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01 MAY-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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       REFERENCE
AUTHORS
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AUTHORS
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AUTHORS
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TITLE

COMMENT

JOURNAL TITLE

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* NOTE: Estimated insert size may differ from sequence length

(see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* In 172927. contig of 172927 bp in length.

Location/Qualifiers
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may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                        580 TAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGT
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                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
6.1%; Score 59.6; DB 2;
Best Local Similarity 52.4%; Pred. No. 0.00021;
Matches 131; Conservative 0; Mismatches 119;
                                                                                                                                              Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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clone_end:Sp6"
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172320 AGCATGTATCAGCACTGTATCAGCACTGTTGTAGCATGTTT 172261
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⁸²⁰ AGTCGTAACA 829 | | | | | | | | 1 172200 TGGTATAACA 172191

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